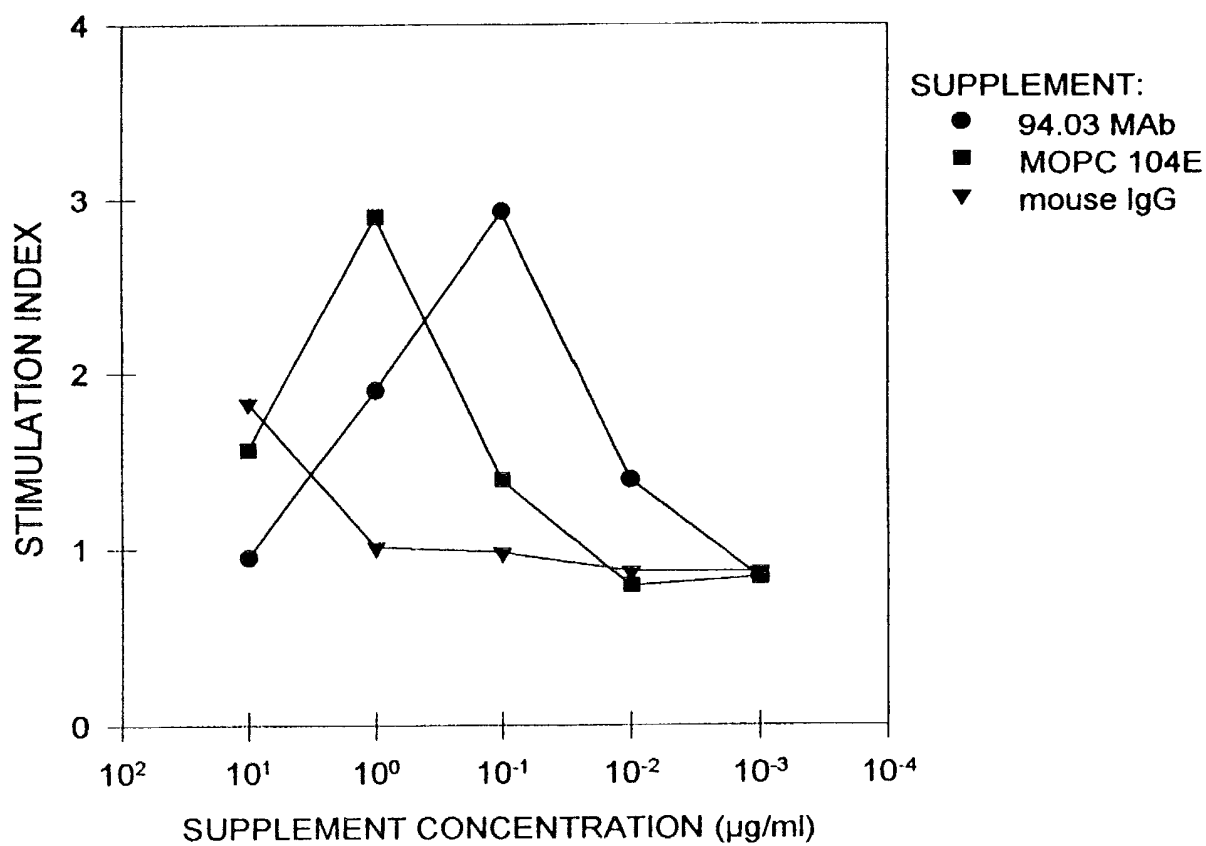




FIG. 1



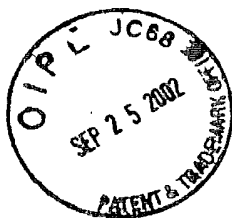


FIG. 2

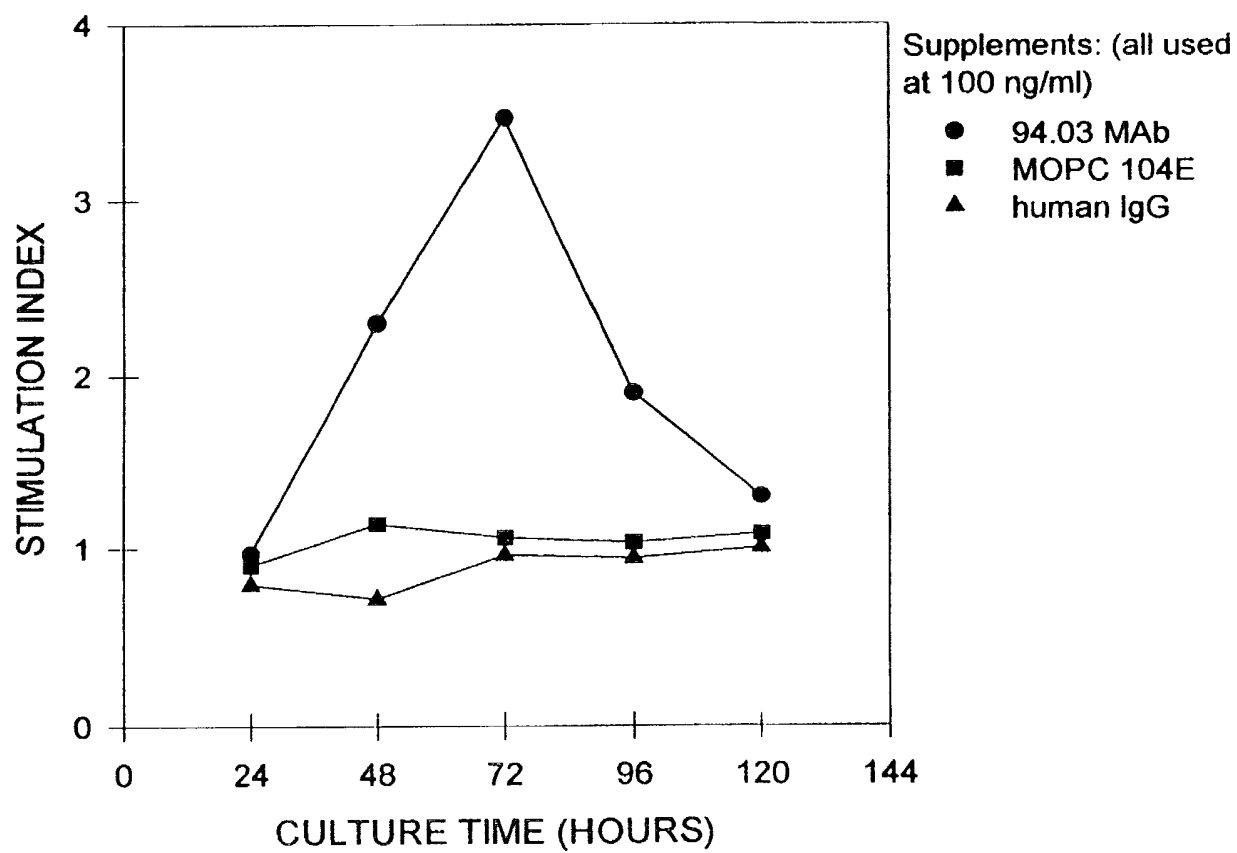


FIG. 3B

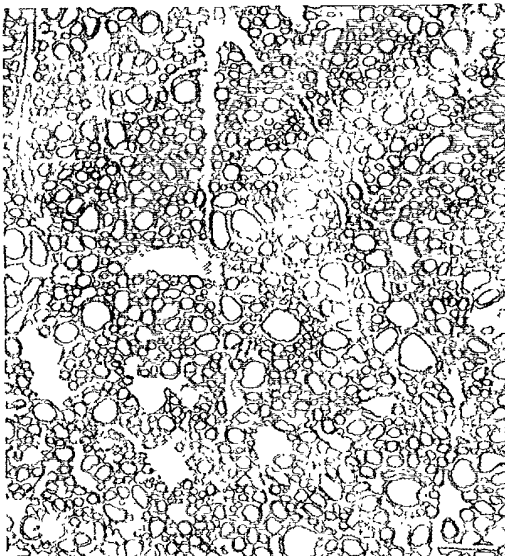
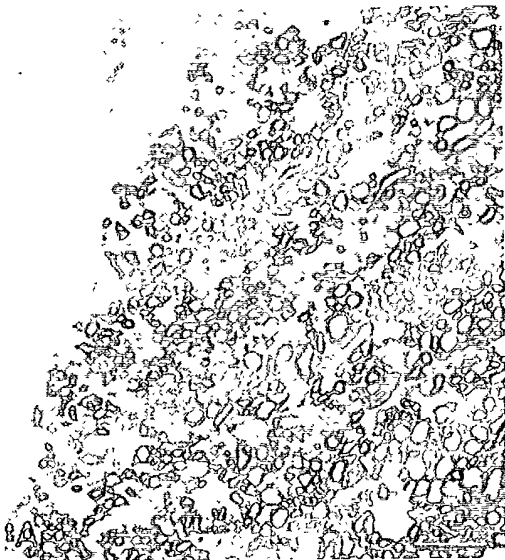


FIG. 3C

FIG. 3D

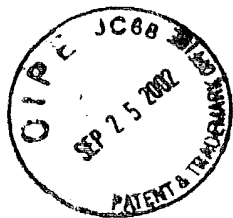


FIG. 5

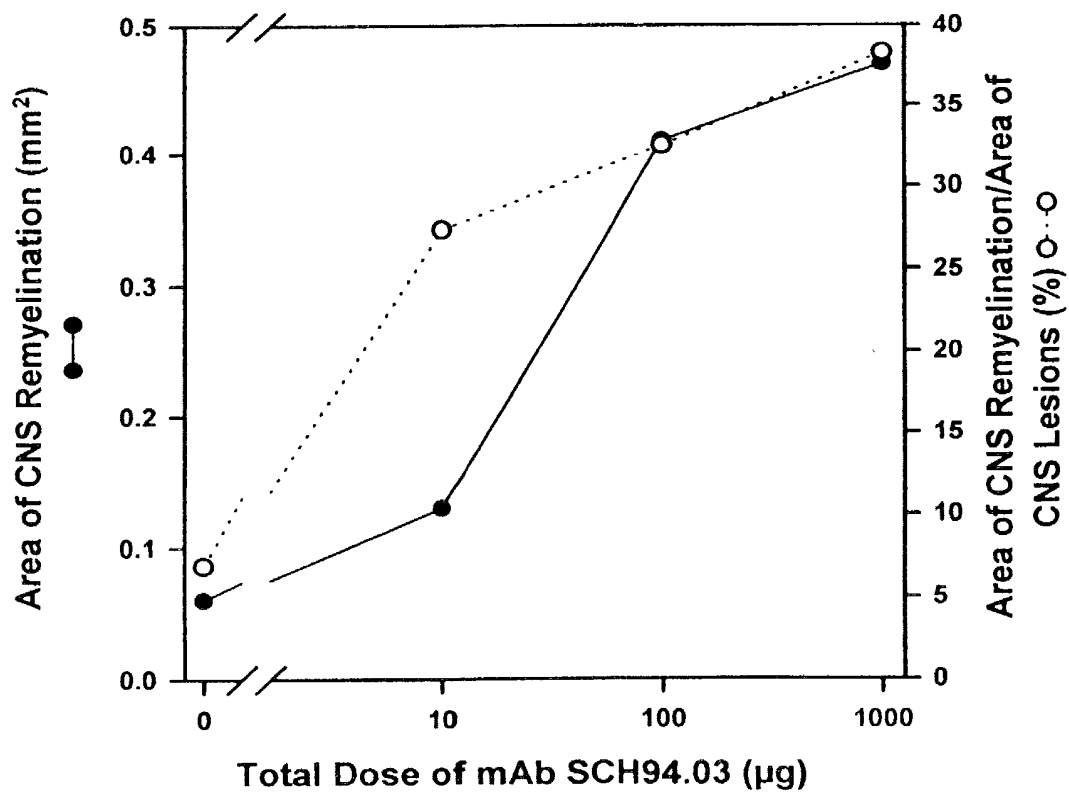


FIG. 6

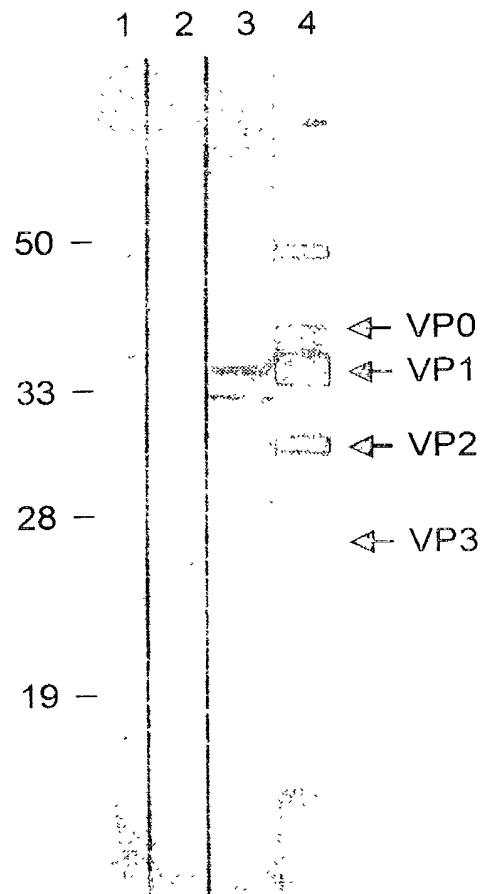


FIG. 7A

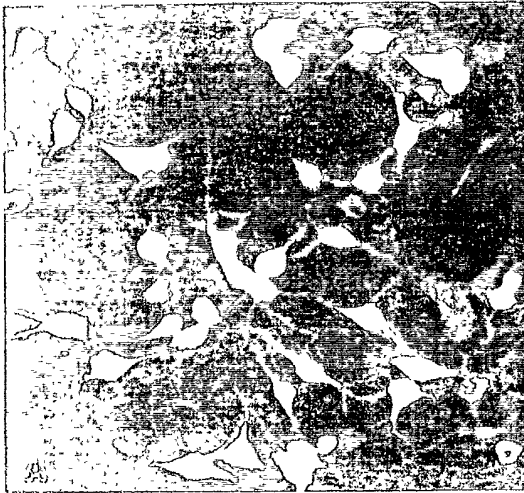


FIG. 7B

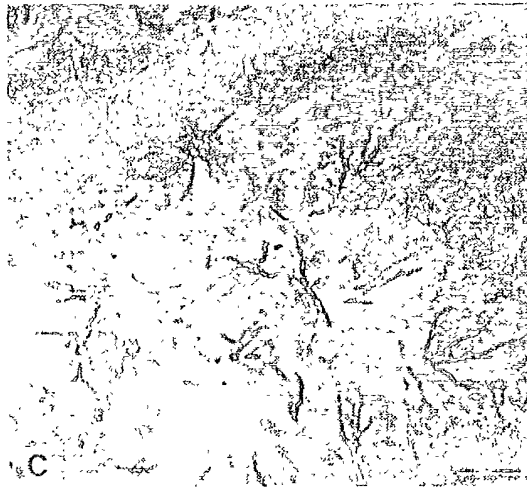
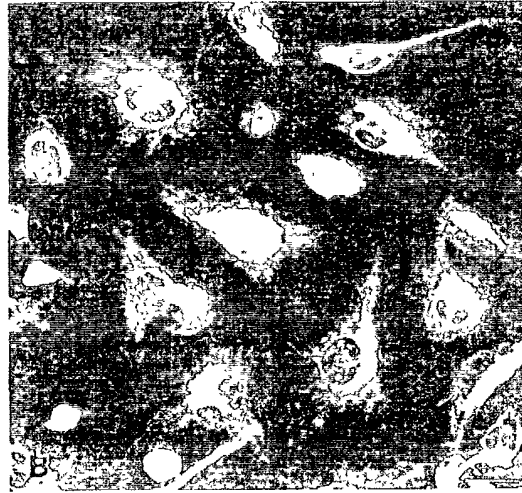


FIG. 7C

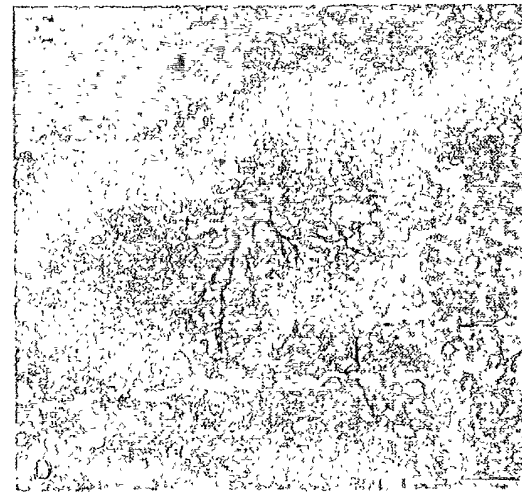
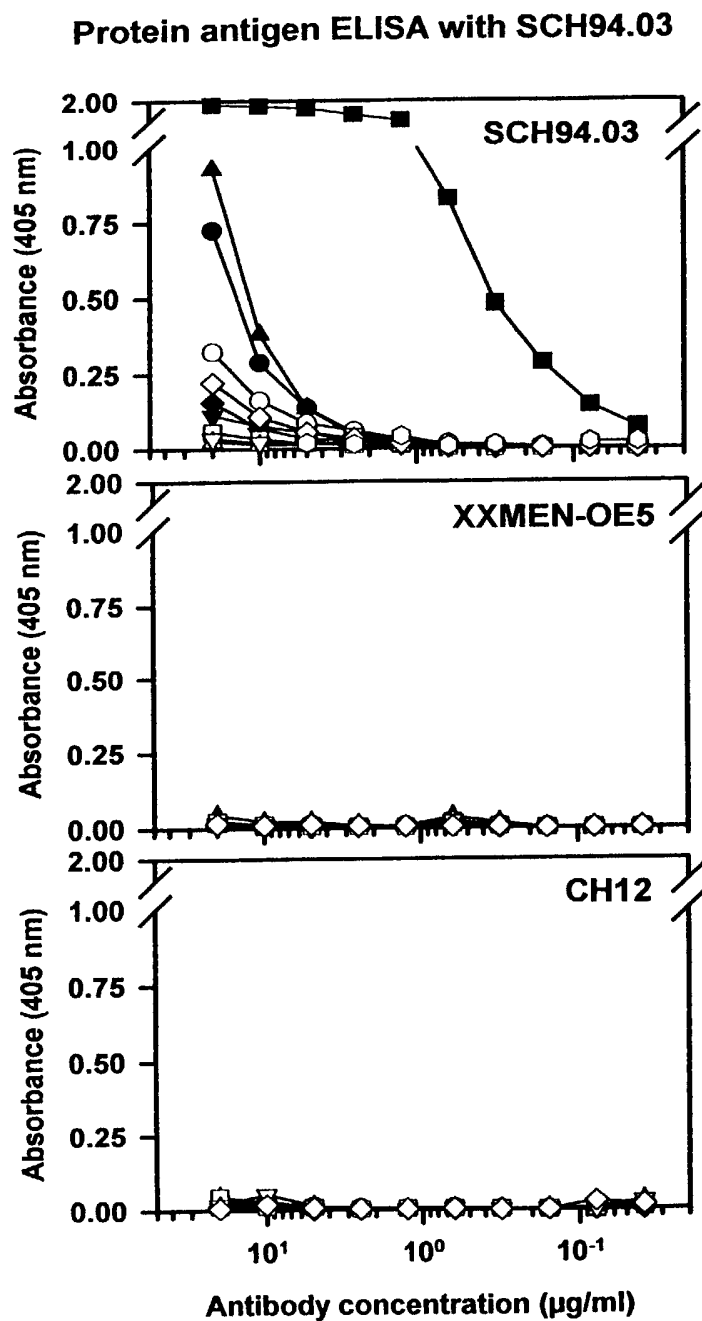


FIG. 7D

FIG. 8A

FIG. 8B

FIG. 8C



Antigen:

- | | |
|-----------------|---------------|
| ● KLH | ○ actin |
| ■ spectrin | □ lysozyme |
| ▲ hemoglobin | △ transferrin |
| ▼ vimentin | ▽ myosin |
| ◆ thyroglobulin | ◇ tubulin |



FIG. 9

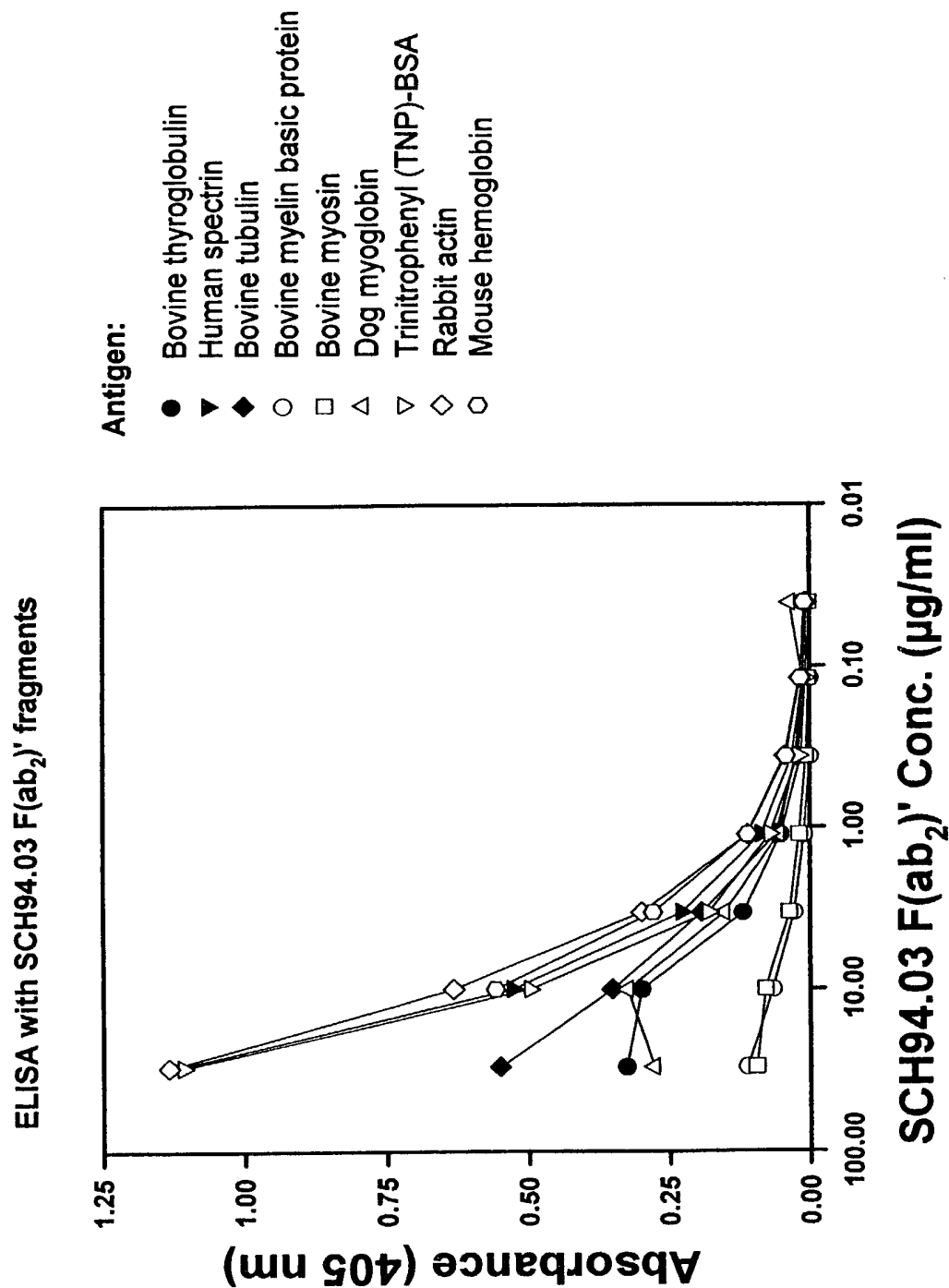


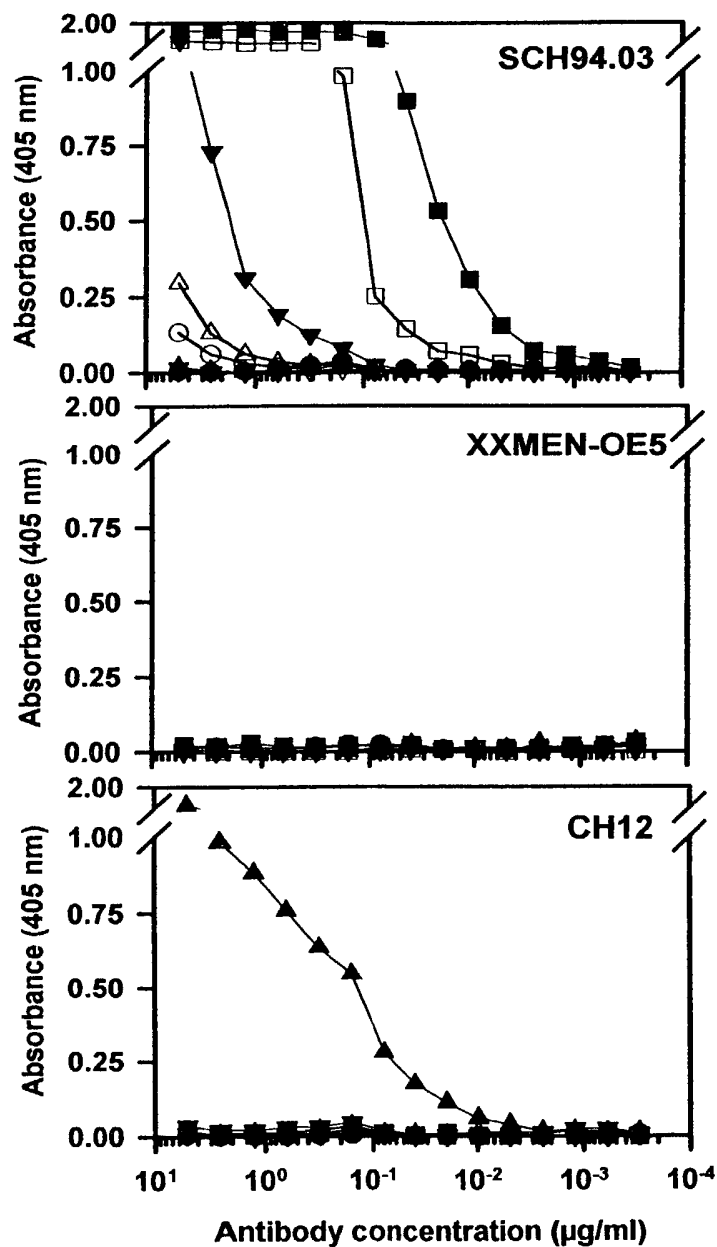


FIG. 10A

FIG. 10B

FIG. 10C

Chemical hapten ELISA with SCH94.03



Hapten:

- none
- FL
- ▲ TMA
- ▼ PhOx
- Ars
- NP
- △ TNP
- ▽ PC

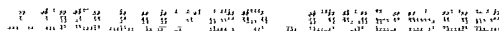


FIG. 11B

			-9					1														
M	G	I	L	F	L	V	A	A	T	G	V	H	S	Q	V	Q	L	Q	Q	P	G	
ATG	GGA	TGT	ATC	CTC	TTT	TTG	GTA	GCA	GCT	ACA	GGT	GTC	CAC	TCC	CAG	GTC	CAA	CTG	CAG	CAG	CCT	GGG

germline V23

	10		20		30																					
T	E	L	V	K	P	G	A	S	V	K	L	S	C	K	A	S	G	Y	T	F	T	S	Y	W	M	H
ACT	GAA	CTG	GTG	ARG	CCT	GGG	GCT	TCA	GTG	ARG	CTG	TCC	TGC	AAG	GCT	TCT	GGC	TAC	ACC	TTC	ACC	AGC	TAC	TGG	ATG	CAC

Jermline V23

[illegible]

germline v23

[illegible]

germline V23

[illegible]

CH12
germline V23
JH2

[illegible]

germline JH2



FIG. 12

		Leader Peptide																				CDR1										CDR2										CDR3										J region										C region																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																		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FIG. 14

Leader Peptide

[illegible]



FIG. 15

Leader Peptide																														
		-4				+1																								
MOPC21 01/04 E7	-19	M	E	S	Q	T	L	V	F	I	S	I	L	L	W	L	Y	G	A	D	G	N	I	V	M	T	Q	S	P	
		ATG	GAA	TCA	CAG	ACT	CTG	GTC	TTC	ATA	TCC	ATA	CTG	CTC	TGG	TTA	TAT	GGA	GCT	GAT	GGG	AAC	ATT	GTA	ATG	ACC	CAA	TCT	CCC	
		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
MOPC21 01/04 E7	10	K	S	M	S	M	S	V	G	E	R	V	T	L	T	C	K	A	S	E	N	V	V	T	Y	Y	S	S	W	Y
		AAA	TCC	ATG	TCC	ATG	TCA	GTA	GGA	GAG	AGG	GTC	ACC	TTG	ACC	TGC	AAG	GCC	AGT	GAG	AAT	GTG	GTG	ACT	TAT	GTT	TCN	TGG	TAT	
		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
MOPC21 01/04 E7	40	Q	Q	K	P	E	Q	S	P	K	L	L	I	Y	G	A	S	N	R	Y	T	G	G	V	P	D	R	F	T	G
		CAA	CAG	AAA	CCA	GAG	CAG	TCT	CCT	AAA	CTG	CTG	ATA	TAT	GGG	GCA	TCC	AAC	CGG	TAC	ACT	GGG	GTC	CCN	GAT	CGC	TTC	ACA	GGC	
		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
MOPC21 01/04 E7	70	S	G	S	A	T	D	F	T	L	T	I	S	S	V	Q	A	E	D	L	A	D	Y	H	C	TGT	GGA	Q	G	Y
		AGT	GGA	TCT	GCA	ACA	GAT	TTC	ACT	CTG	ACC	ATC	AGC	AGT	GTG	CAG	GCT	GAA	GAC	CTT	GCA	GAT	GAT	TAT	CAC	TGT	GGA	CAG	GGT	TAC
		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
MOPC21 01/04 E7	100	S	Y	P	Y	T	F	G	G	G	T	K	L	E	I	K	R	CGG	GCT	GAT	GCT	TCA								
		AGC	TAT	CCG	TAC	ACG	TTC	GGA	GGG	GGG	ACC	AAG	CTG	GAA	ATA	AAA	CGG	GCT	GAT	GCT	TCA									
		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

CDR1

30

CDR2

50

60

CDR3

80

90

C region

J region

CDR3

106

106A

100

MOPC21
germline Jx2
01/04
E7



FIG. 17

Leader Peptide

												-4				+1											
M	M	E	S	Q	I	Q	V	F	V	F	V	L	W	L	S	G	V	D	G	D	I	V	M	T	Q	S	H
ATG	GAG	TCA	CAG	ATT	CAG	GTC	TTT	GTA	TTC	GTG	TTT	CTC	TGG	TTG	TCT	GGT	GTT	GAC	GGA	GAC	ATT	GTG	ATG	ACC	CAG	TCT	CAC

CDR1

[illegible]

CDR2

Q Q K P G Q S P K L L I Y S A S Y R Y T G V P D R F T G
CAA CAG AAA CCA GGA CAA TCT CCT AAA CTA CTG ATT TAC TCG GCA TTC TAC CGG TAC ACT GGA GTC CCT GAT GGC

CDR3

70										80										90									
S	G	S	G	T	D	F	T	F	T	I	S	S	V	Q	A	E	D	L	A	V	Y	Y	C	Q	Q	H	Y		
AGT	GGA	TCT	GGG	ACG	GAT	TTC	ACT	TTC	ACC	ATC	AGC	AGT	GTG	CAG	GCT	GAA	GAC	CTG	GCA	GTT	TAT	TAC	TGT	CAG	CAA	CAT	TAT		

CDR3

C region

J region

[illegible]

Timeline Jx5
B5



FIG. 18

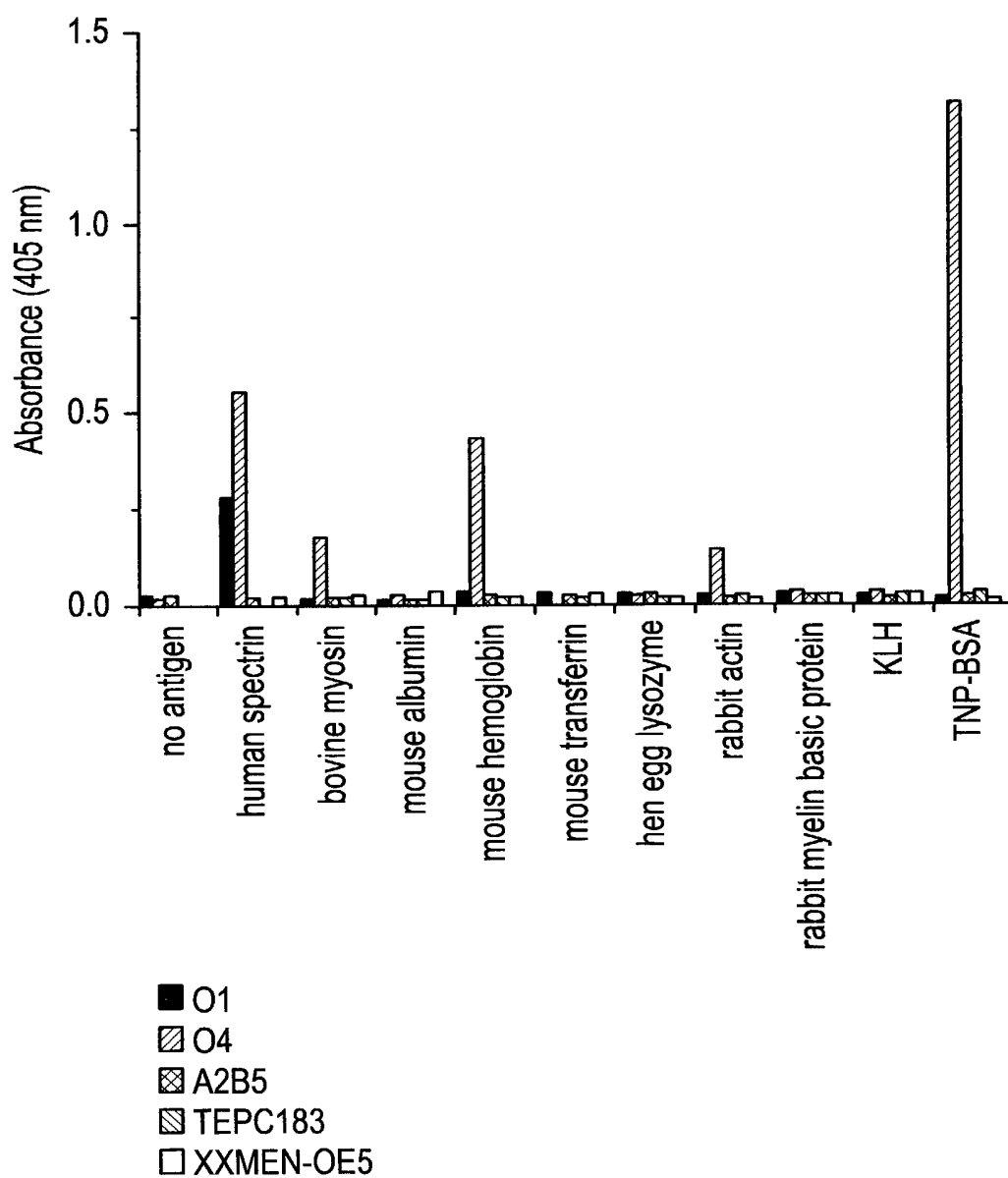


FIG. 19A

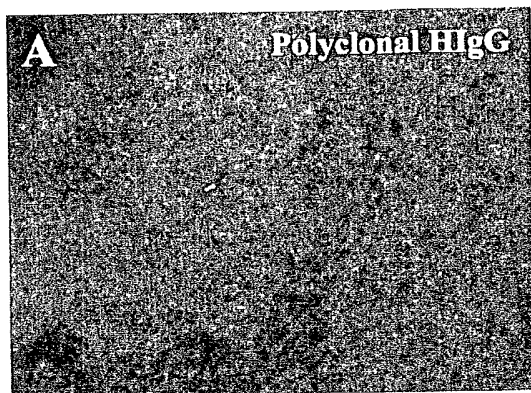


FIG. 19B

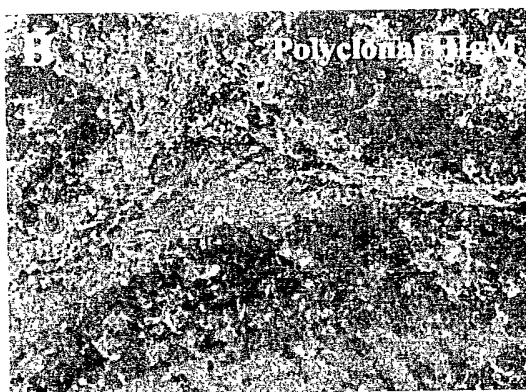


FIG. 19C



FIG. 19D

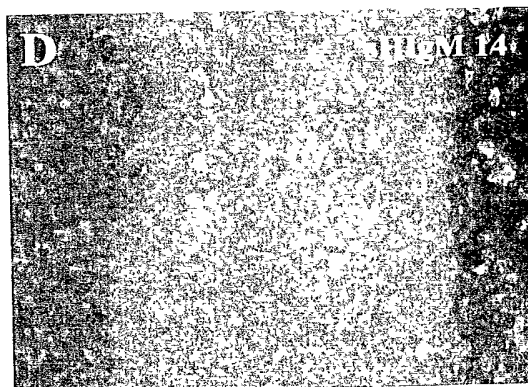


FIG. 19E

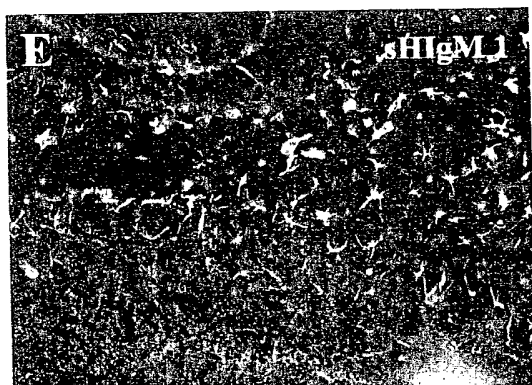


FIG. 19F

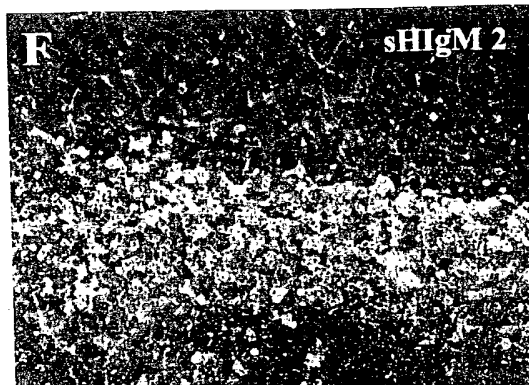


FIG. 20A

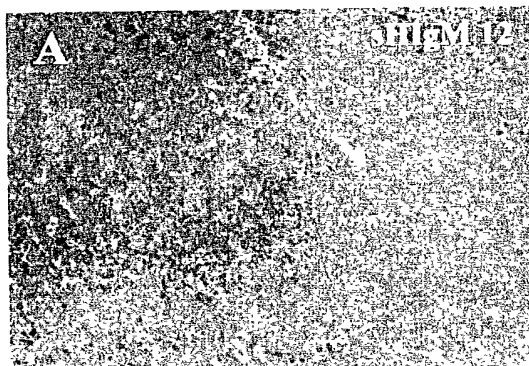


FIG. 20B



FIG. 20C



FIG. 20D

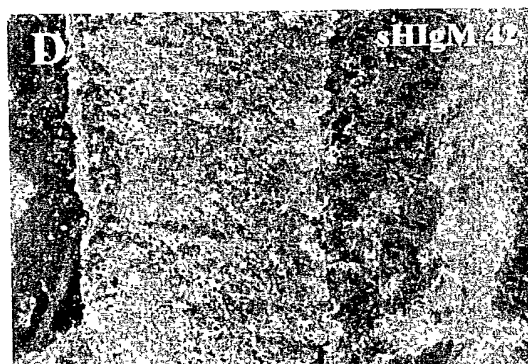


FIG. 20E



FIG. 20F



FIG. 21A

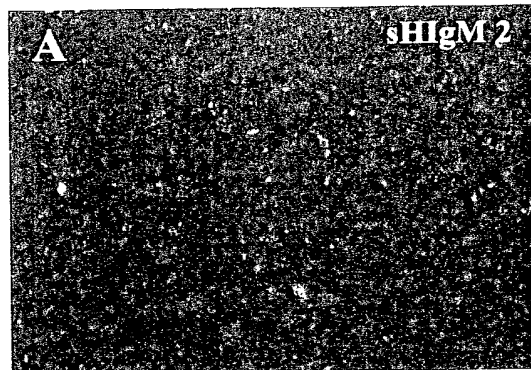


FIG. 21B

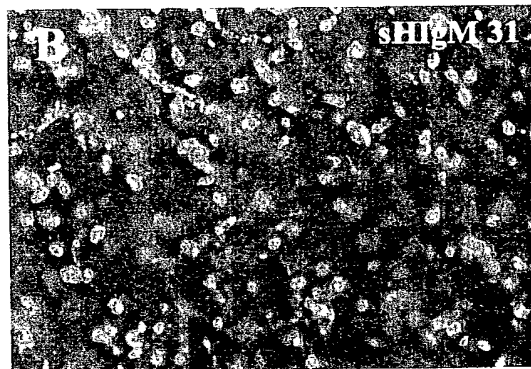


FIG. 21C

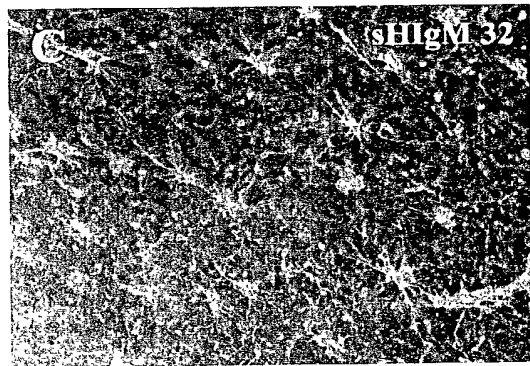


FIG. 21D

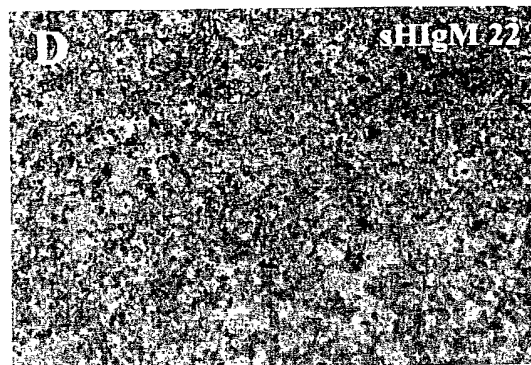


FIG. 21E



FIG. 22A



FIG. 22B



FIG. 22C



FIG. 22D

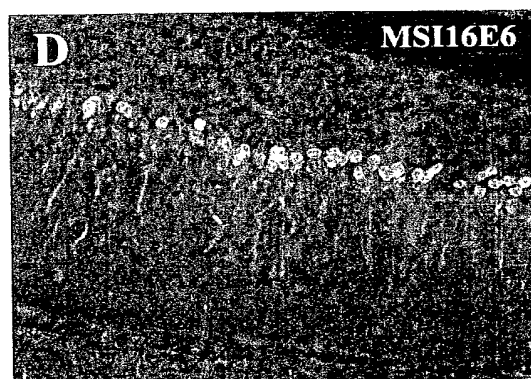


FIG. 22E

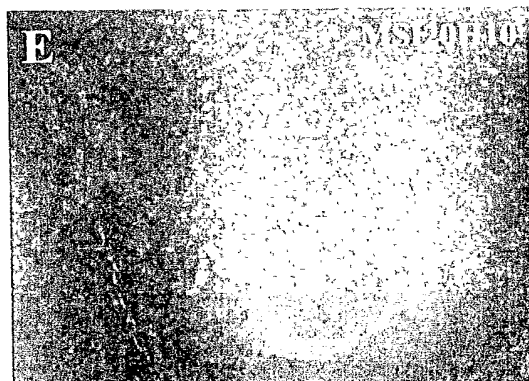


FIG. 22F

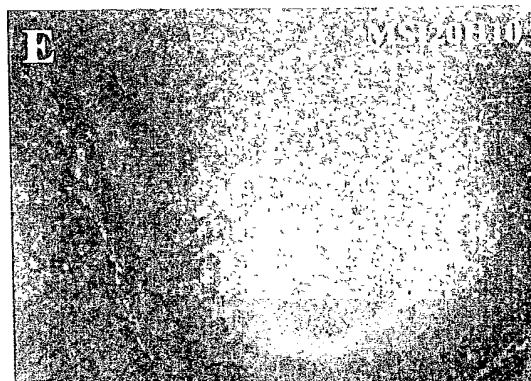


FIG. 23B

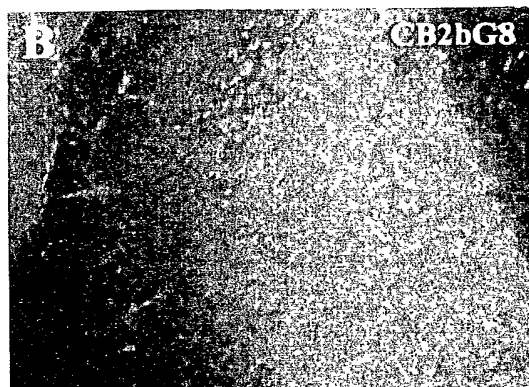


FIG. 23D



FIG. 23F



A high-contrast, black and white image showing a dense, textured surface, possibly a microscopic view of a material or a close-up of a rough surface. The image is heavily degraded with horizontal lines and noise, suggesting it is a scan of a physical document.

A high-contrast, black and white image showing a dense, textured surface, possibly a book cover or a heavily patterned fabric. The texture is composed of many small, irregular shapes and lines, creating a complex, almost abstract pattern. The overall appearance is grainy and noisy, with a dark background and lighter, irregular highlights.

sHlgM 2

FIG. 25A

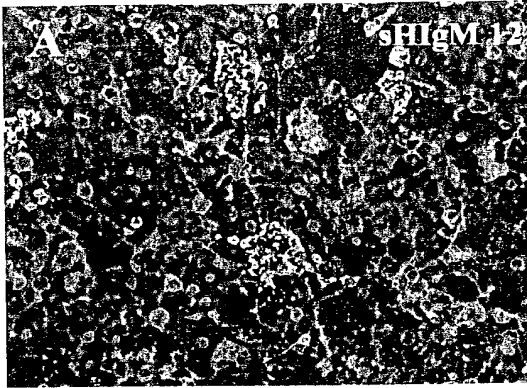


FIG. 25B

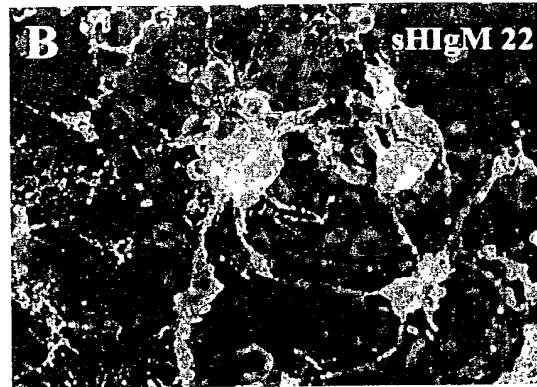


FIG. 25C

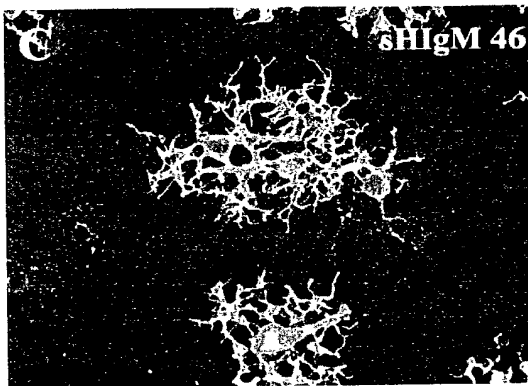


FIG. 25D

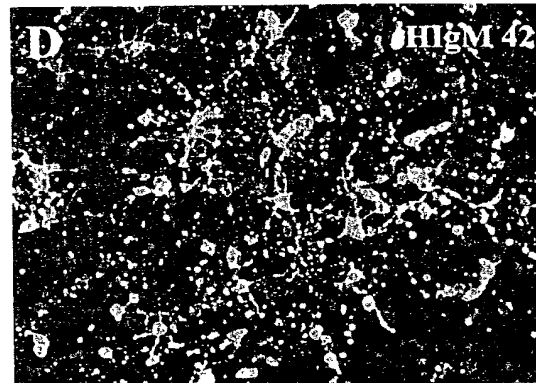


FIG. 25E

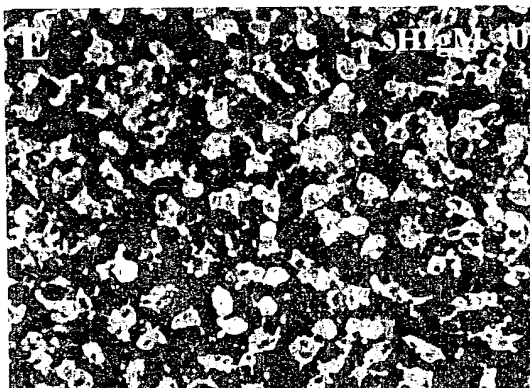
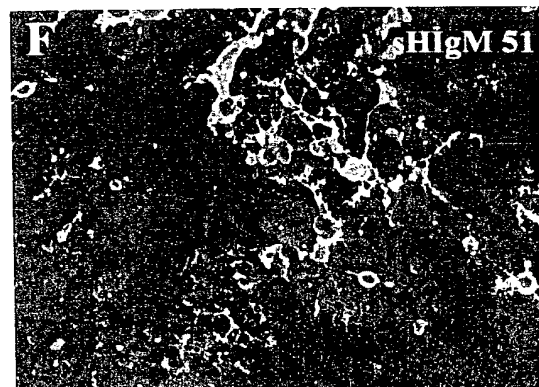


FIG. 25F



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09/25/02

FIG. 26A

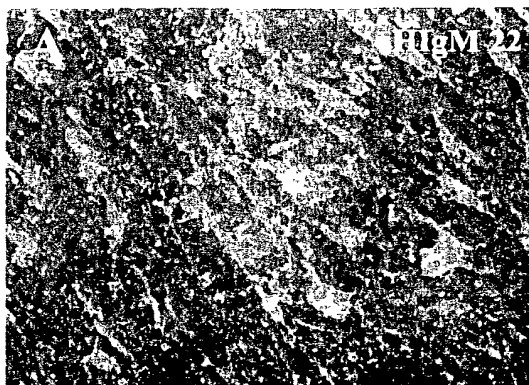


FIG. 26B

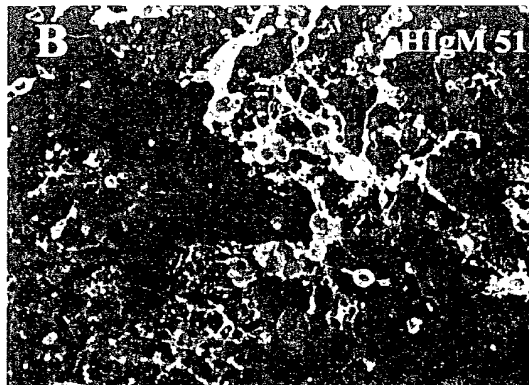


FIG. 26C

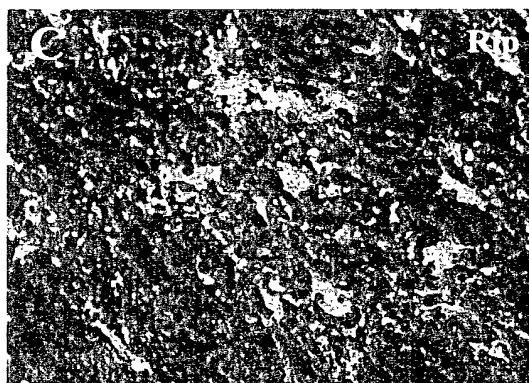


FIG. 26D

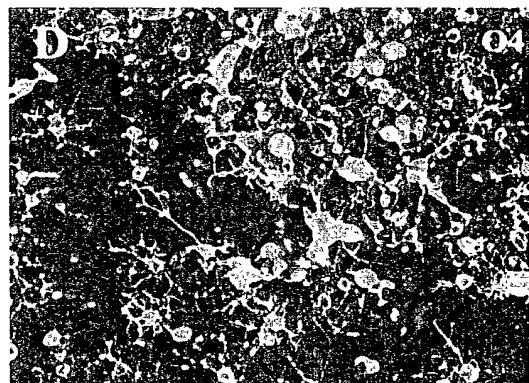


FIG. 26E

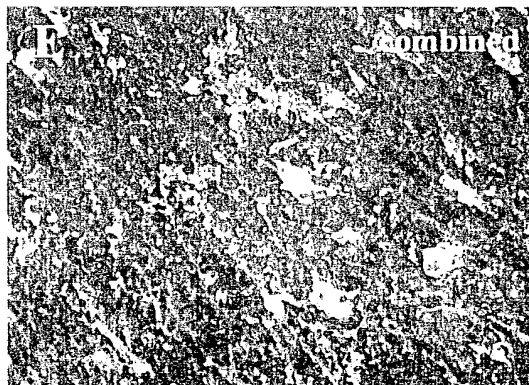
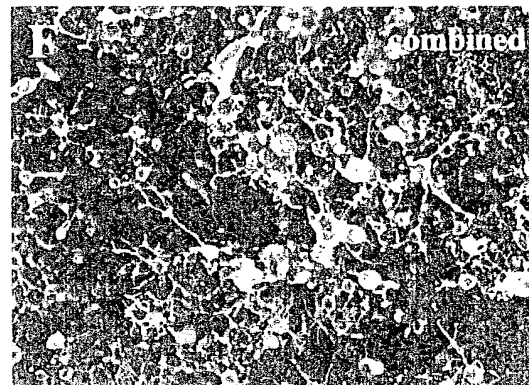


FIG. 26F



[illegible]

MSI19E5

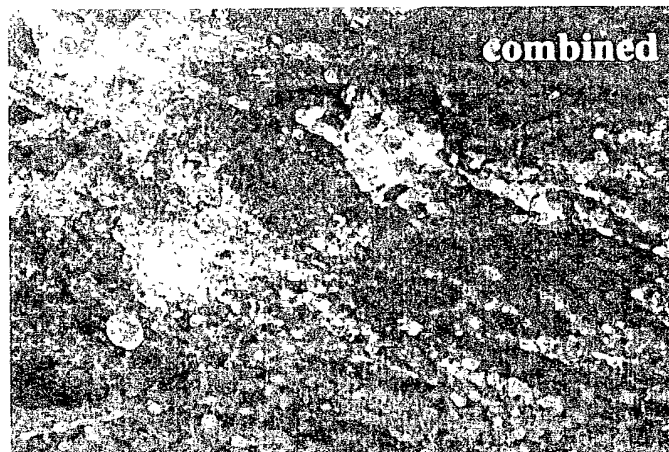
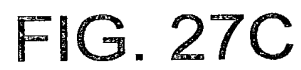
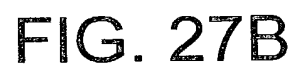




FIG. 29

ebvHlgMs Characterized by Binding to SCH via ELISA

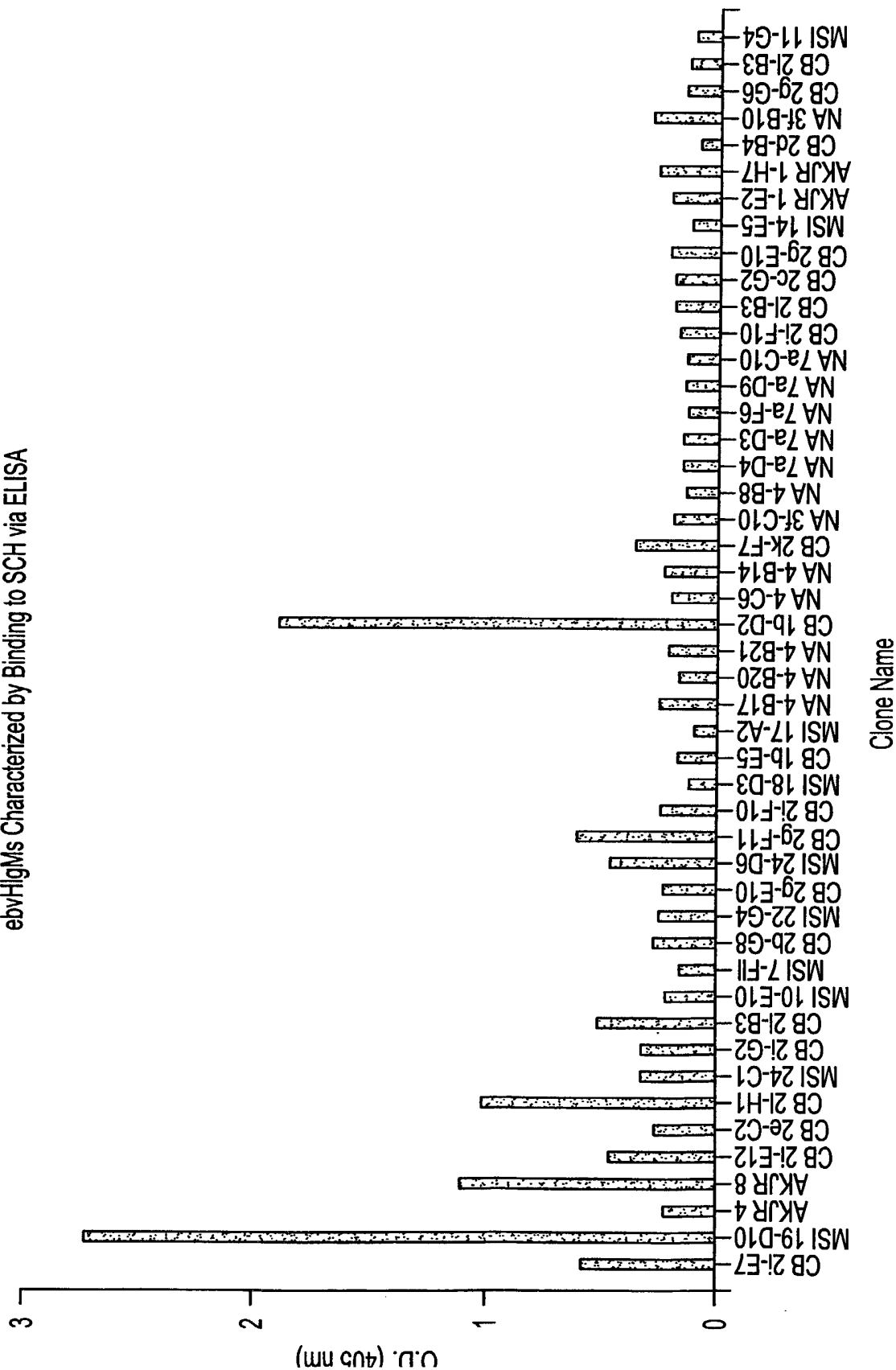


FIG. 30A

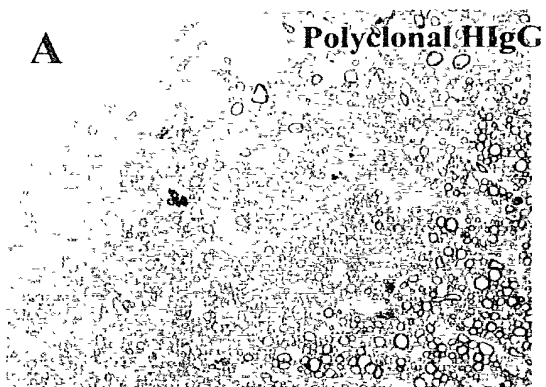


FIG. 30B

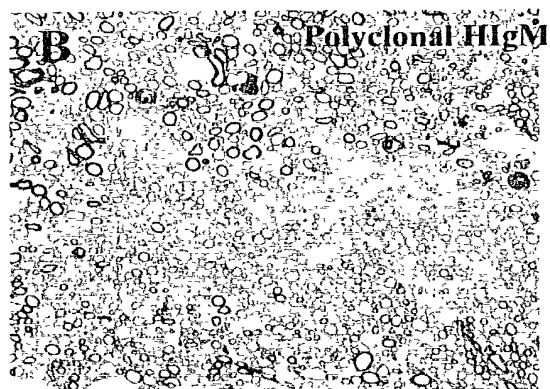


FIG. 30C



FIG. 30D



FIG. 30E

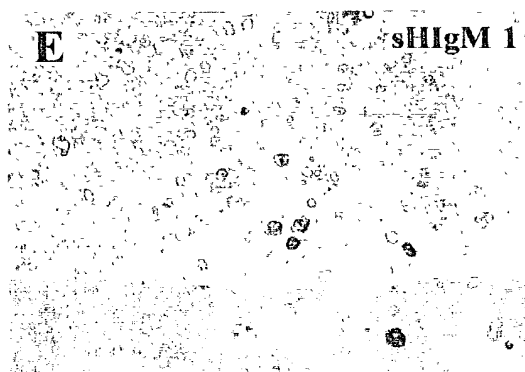
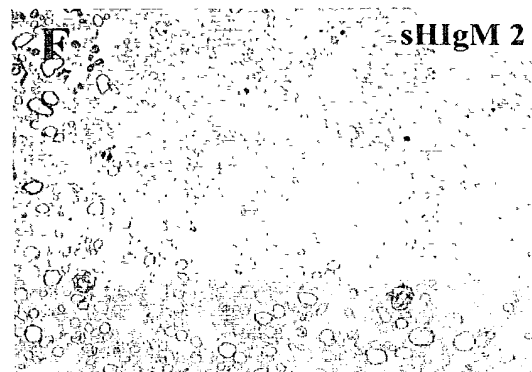


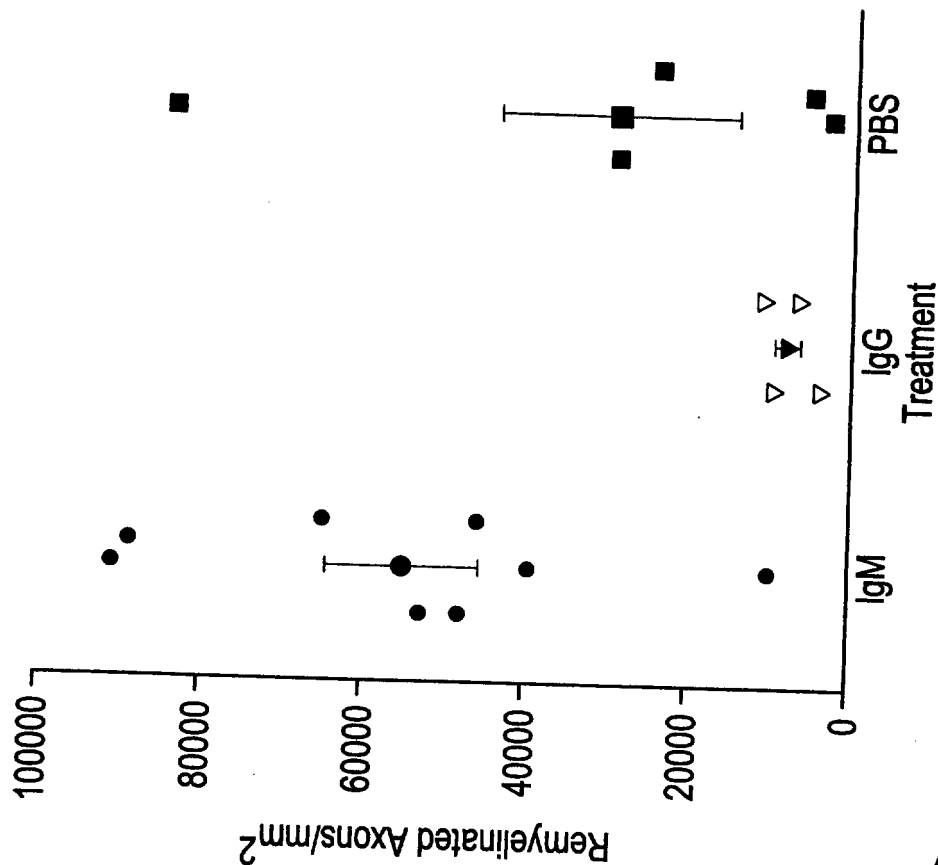
FIG. 30F



This electron micrograph, labeled 'B' in the top left and 'AKJR4' in the top right, shows a cell with a large, dark nucleus containing a prominent nucleolus. The cytoplasm is filled with numerous small, dark, circular granules, likely representing ribosomes or small vesicles. The overall texture is granular and dense.

FIG. 32

Lysolecithin Experiment 21 Day Experiment



ANIMAL #	STRAIN	RX	DAY RX	Axons/mm ²
1091-98	SJL	HUMAN IGM	7	47881.04
1093-98	SJL	HUMAN IGM	7	90745.80
1094-98	SJL	HUMAN IGM	7	88638.09
1095-98	SJL	HUMAN IGM	7	52767.82
1181-98	SJL	HUMAN IGM	7	45583.42
1182-98	SJL	HUMAN IGM	7	39289.31
1183-98	SJL	HUMAN IGM	7	64636.39
1184-98	SJL	HUMAN IGM	7	9937.24
Mean				54934.89
SEM				9376.95
1135-98	SJL	HUMAN IGG	7	9433.96
1139-98	SJL	HUMAN IGG	7	3702.92
1140-98	SJL	HUMAN IGG	7	11028.19
1141-98	SJL	HUMAN IGG	7	6493.06
Mean				7664.53
SEM				1620.49
1122-98	SJL	PBS	7	2457.22
1124-98	SJL	PBS	7	23746.34
1170-98	SJL	PBS	7	83549.17
1171-98	SJL	PBS	7	4819.92
1172-98	SJL	PBS	7	28878.82
Mean				28690.29
SEM				14649.14

SCANNED 24



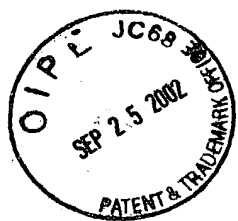
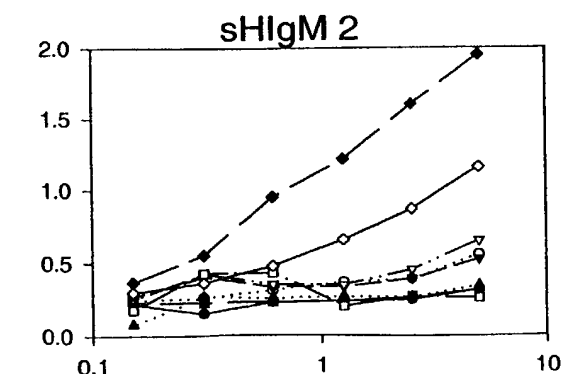
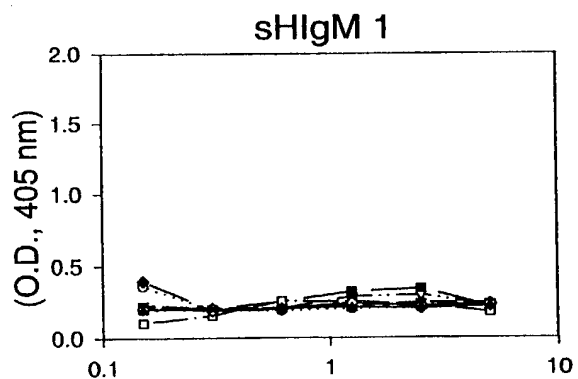
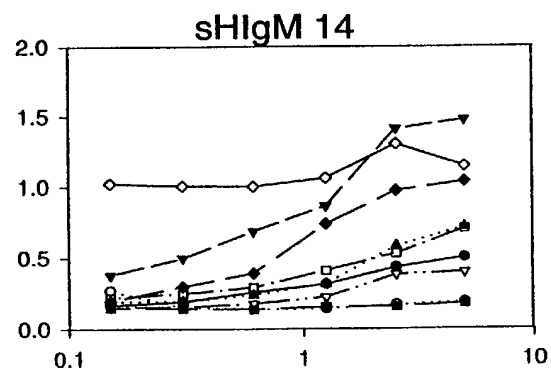
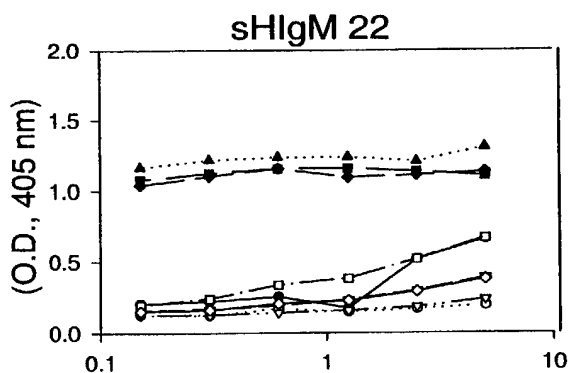
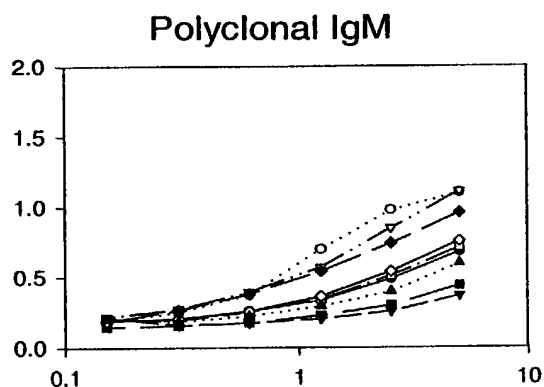
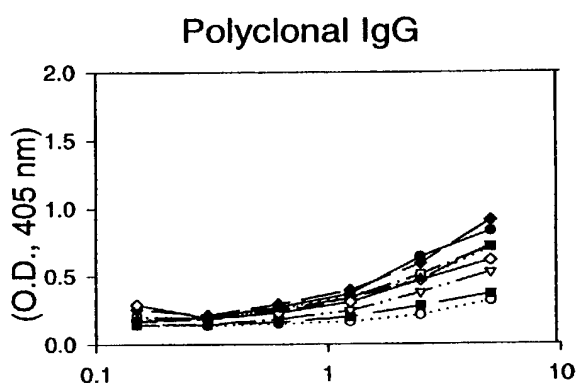


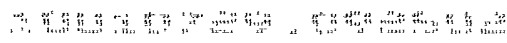
FIG. 33

Hapten Elisa

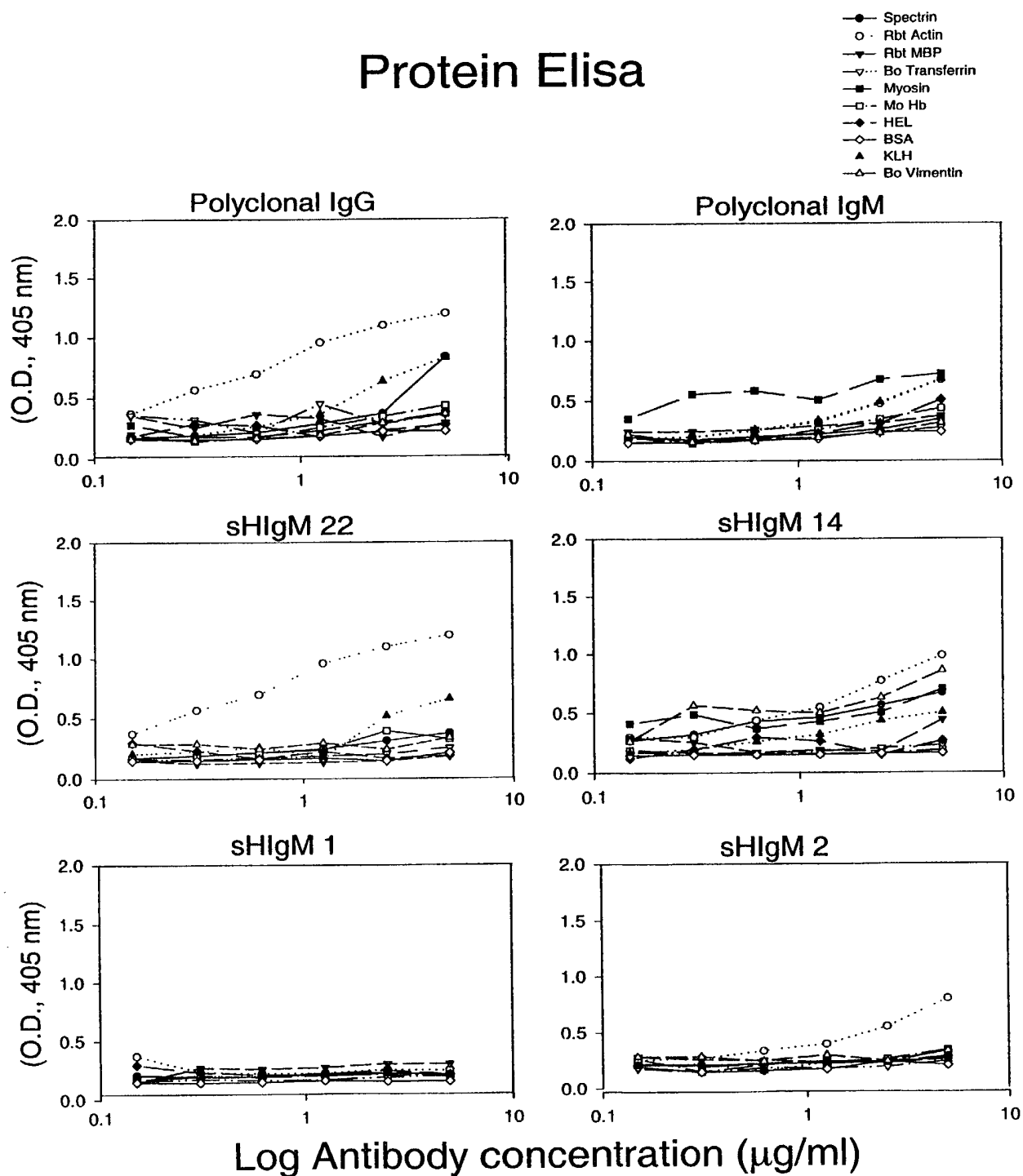
- KLH
- TMA
- ▼ ARS
- ▽ PC
- TNP
- PhoX
- ◆ NP
- ◇ FITC
- ▲ DNP



Log Antibody concentration ($\mu\text{g/ml}$)



Protein Elisa



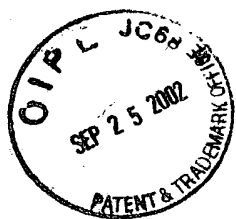


FIG. 35

/FR1-----
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15
O V O L V E S G G G V V O P G
CAG GTG CAG CTG GTG GAG TCT GGG GGA GGC GTG GTC CAG CCT GGG
Clone A sH-IgM.22 VH G
Clone B sH-IgM.22 VH

16 17 18 19 20 21 22 23 24 25 26 27 28 29 30
R S L R L S C A A S G F T F S
AGG TCC CTG AGA CTC TCC TGT GCA GCC TCT GGA TTC ACC TTC AGT

/CDR1-----/FR2-----
31 32 33 34 35 36 37 38 39 40 41 42 43 44 45
S S G M H W V R Q A P G K G L
AGC TAT GGC ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGG CTG
C
C

/CDR2-----
46 47 48 49 50 51 52 52A 53 54 55 56 57 58 59
E W V A V(I) I S Y D G S R K Y Y
GAG TGG GTG GCA GTT ATA TCA TAT GAT GGA AGT AAT AAA TAC TAT
T
A C T
GG
GG

/FR3-----
60 61 62 63 64 65 66 67 68 69 70 71 72 73 74
A D S V K G R F T I S R D N S
GCA GAC TCC GTG AAG GGC CGA TTC ACC ATC TCC AGA GAC AAT TCC
C
C

75 76 77 78 79 80 81 82 82A 82B 82C 83 84 85 86
K N T L Y L O M N S L T A D(E) D
AAG AAC ACG CTG TAT CTG CAA ATG AAC AGC CTG AGA GCT GAG GAC
T
T C
CG
C

/CDR3-----
87 88 89 90 91 92 93 94 95 96 97 98 99 100 100A
T A V Y Y C A K G V T G S P T
ACG GCT GTG TAT TAC TGT GCG AAA GAG GTG ACT GCT ATT CCC TAC
T
GA
GA
G
G
G
G
ACG
ACG

/FR4-----
100B 101 102 103 104 105 106 107 108 109 110 111 112 113
L D Y W G O G T L V T V S S
TTT GAC TAC TGG GGC CAG GGA ACC CTG GTC ACC GTC TCC TCA
C
C
G
G

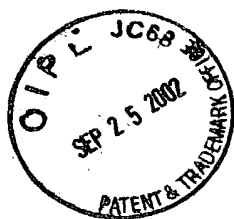


FIG. 36

/FR1-----															
1	2	3	4	5	6	7	8	9	11	12	13	14	15	16	
O	S	V	L	T	O	P	P	S	V	S	A	A	P	G	
CAG	TCT	GTG	TTG	ACG	CAG	CCG	CCC	TCA	GTG	TCT	GCG	GCC	CCA	GGA	
Clone I sH-IgM.22 Vλ					G		T				T				
Clone II sH-IgM.22 Vλ					G		T				T				
-----/CDR1-----															
17	18	19	20	21	22	23	24	25	26	27	27A	27B	28	29	
O	K	V	T	I	S	C	S	G	S	S	S	N	I	G	
CAG	AAG	GTC	ACC	ATC	TCC	TGC	TCT	GGA	AGC	AGC	TCC	AAC	ATT	GGG	
														C	
														C	
-----/FR2-----															
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	
N	N	F	V	S	W	Y	O	O	L	P	G	T	A	P	
AAT	AAT	TAT	GTA	TCC	TGG	TAC	CAG	CAG	CTC	CCA	GGA	ACA	GCC	CCC	
		T						A							
		T						A							
-----/CDR2-----/FR3-----															
45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	
R(K)	L	L	I	Y	D	I	T	K	R	P	S	G	I	P	
AAA	CTC	CTC	ATT	TAT	GAC	AAT	AAT	AAG	CGA	CCC	TCA	GGG	ATT	CCT	
G						T	C								
						T	C								

60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	
D	R	F	S	G	S	K	S	G	T	S	A	T	L	G	
GAC	CGA	TTC	TCT	GGC	TCC	AAG	TCT	GGC	ACG	TCA	GCC	ACC	CTG	GGC	
-----/CDR3-----															
75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	
I	T	G	L	O	T	G	D	E	A	D	Y	Y	C	G(E)	
ATC	ACC	GGA	CTC	CAG	ACT	GGG	GAC	GAG	GCC	GAT	TAT	TAC	TGC	GGA	

-----/FR4-----															
90	91	92	93	94	95	95A	95B	96	97	98	99	100	101	102	
T	W	D	S	S	L	S	A	V	V	F	G	G	G	T	
ACA	TGG	GAT	AGC	AGC	CTGT	GTG	GTA	TTC	GGC	GGA	GGG	ACC	
						AGT	GC					G			
						AGT	GC					G			
-----/Cλ-----															
103	104	105	106	106A	107	108	109	110							
K	L	T	V	L	G	O	P	K							
AAG	CTG	ACC	GTC	CTA	GGT	CAG	CCC	AAG							

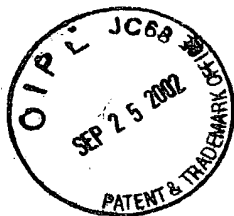


FIG. 37

Sequence of MSI 19-D10 V_H

FR1-----
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16
CAG GTG CAG CTG CAG GAG TCG GGC CCA GGA CTG GTG AAG CCT TCG GAG
Q V Q L Q E S G P G L V K P S E

-----/CDR1
17 18 19 20 21 22 23 24 25 26 27 28 29 30 31
ACC CTG TCC CTC ACC TGC ACT GTC TCT GGT GGC TCC ATC AGT AGT
T L S L T C T V S G G S I S S

-----/FR2-----
32 33 34 35 36 37 38 39 40 41 42 43 44 45 46
TAC TAC TGG AGC TGG ATC CGG CAG CCC CCA GGG AAG GGA CTG GAG
Y Y W S W I R Q P P G K G L E

-----/CDR2-----
47 48 49 50 51 52 53 54 55 56 57 58 59 60 61
TGG ATT GGG TAT ATC TAT TAC AGT GGG AGC ACC AAC TAC AAC CCC
W I G Y I Y Y S G S T N Y N P

-----/FR3-----
62 63 64 65 66 67 68 69 70 71 72 73 74 75 76
TCC CTC AAG AGT CGA GTC ACC ATA TCA GTA GAC ACG TCC AAG AAC
S L K S R V T I S V D T S K N

77 78 79 80 81 82 82A 82B 82C 83 84 85 86 87 88
CAG TTC TCC CTG AAG CTG AGC TCT GTG ACC GCT GCG GAC ACG GCC
Q F S L K L S S V T A A D T A

-----/CDR3-----
89 90 91 92 93 94 95 96 97 98 99 100 100A100B100C
GTG TAT TAC TGT GCG AGG TCG GCA CAG CAG CAG CTG GTA TAC TAC
V Y Y C A R S A Q Q Q L V Y Y

-----/FR4-----/Cμ-
100D 101 102 103 104 105 106 107 108 109 110 111 112 113 114
TTT GAC TAC TGG GGC CAG GGA ACC CTG GTC ACC GTC TCC TCA GGG
F D Y W G Q G T L V T V S S G

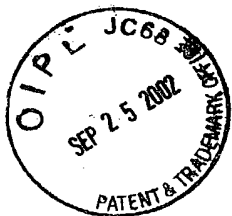


FIG. 38

Sequence of MSI 19-D10 V_K

FR 1-----
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15
GAC ATC GTG ATG ACC CAG TCT CCA GAC TCC CTG GCT GTG TCT CTG
D I V M T Q S P D S L A V S L

-----/CDR1-----
16 17 18 19 20 21 22 23 24 25 26 27 27A 27B 27C
GGC GAG AGG GCC ACC ATC AAC TGC AAG TCC AGC CAG AGT GTT TTA
G E R A T I N C K S S Q S V L

-----/FR2-----
27D 27E 27F 28 29 30 31 32 33 34 35 36 37 38
TAC AGC TCC AAC AAT AAG AAC TAC TTA GCT TGG TAC CAG CAG
Y S S N N K N Y L A W Y Q Q

-----/CDR2-----
39 40 41 42 43 44 45 46 47 48 49 50 51 52 53
AAA CCA GGA CAG CCT CCT AAG CTG CTC ATT TAC TGG GCA TCT ACC
K P G Q P P K L L I Y W A S T

-----/FR3-----
54 55 56 57 58 59 60 61 62 63 64 65 66 67 68
CGG GAA TCC GGG GTC CCT GAC CGA TTC AGT GGC AGC GGG TCT GGG
R E S G V P D R F S G S G S G

69 70 71 72 73 74 75 76 77 78 79 80 81 82 83
ACA GAT TTC ACT CTC ACC ATC AGC AGC CTG CAG GCT GAA GAT GTG
T D F T L T I S S L Q A E D V

-----/CDR3-----/FR4
84 85 86 87 88 89 90 91 92 93 94 95 96 97 98
GCA GTT TAT TAC TGT CAG CAA TAT TAT AGT ACT CCT CTC ACT TTC
A V Y Y C Q Q Y Y S T P L T F

-----/Ck-----
99 100 101 102 103 104 105 106 107 108 109 110 111 112 113
GGC CCT GGG ACC AAA GTG GAT ATC AAA CGA ACT GTG GCT GCA CCA
C D C E V V D T V D A A V V A A A

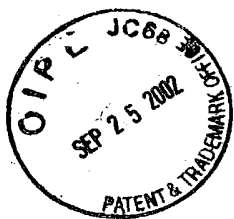


FIG. 39A

Mixed Primary Glia
sH-IgM.22 Ca^{2+} response

- ratio cell #1
- ratio cell #2
- △ sH-IgM.22 ($3\mu\text{g/ml}$)
- ▲ Br-A23187 ($10\mu\text{M}$)

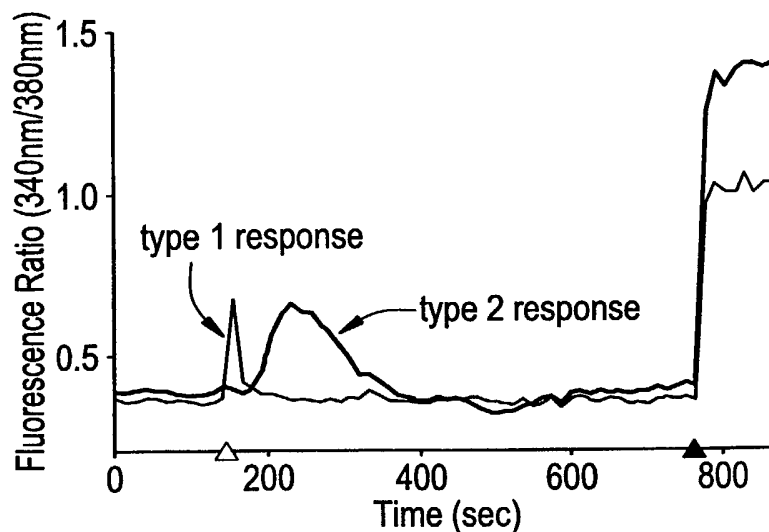


FIG. 39B

Mixed Primary Glia
SCH 94.03 Ca^{2+} response

- ratio cell #1
- ratio cell #2
- △ SCH 94.03 ($3\mu\text{g/ml}$)
- ▲ Br-A23187 ($10\mu\text{M}$)

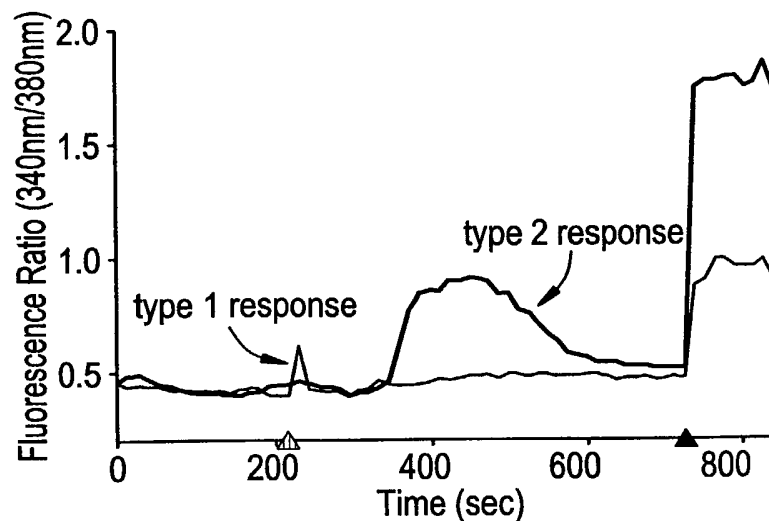


FIG. 39C

Mixed Primary Glia
CH 12/sH-IgM.14 Ca^{2+} response

- ratio cell #1
- ratio cell #2
- △ CH 12 ($3\mu\text{g/ml}$)
- △ sH-IgM.14 ($3\mu\text{g/ml}$)
- ▲ Br-A23187 ($10\mu\text{M}$)

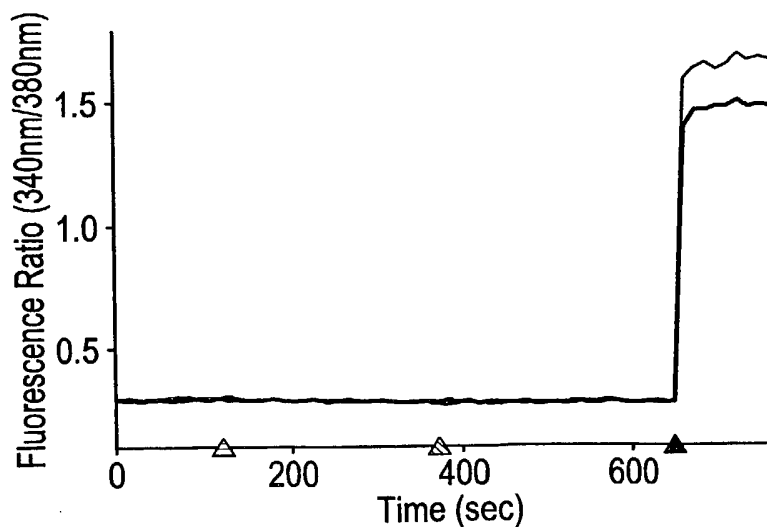


FIG. 41

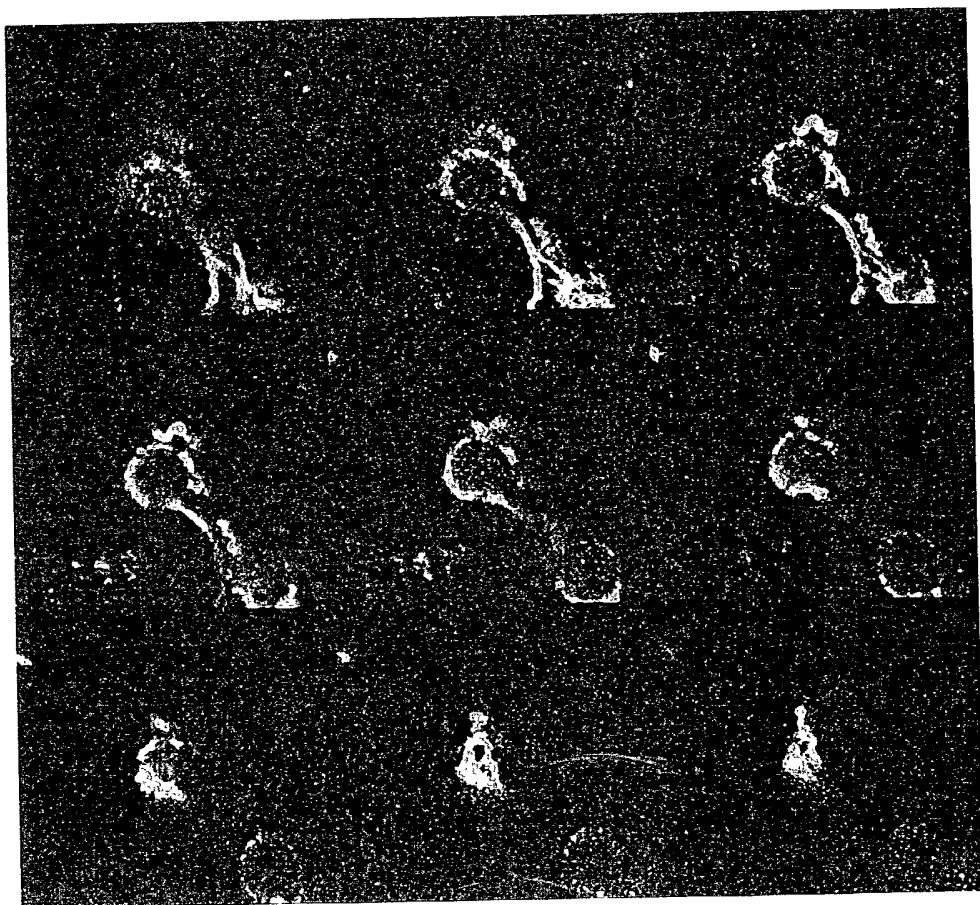


FIG. 42A

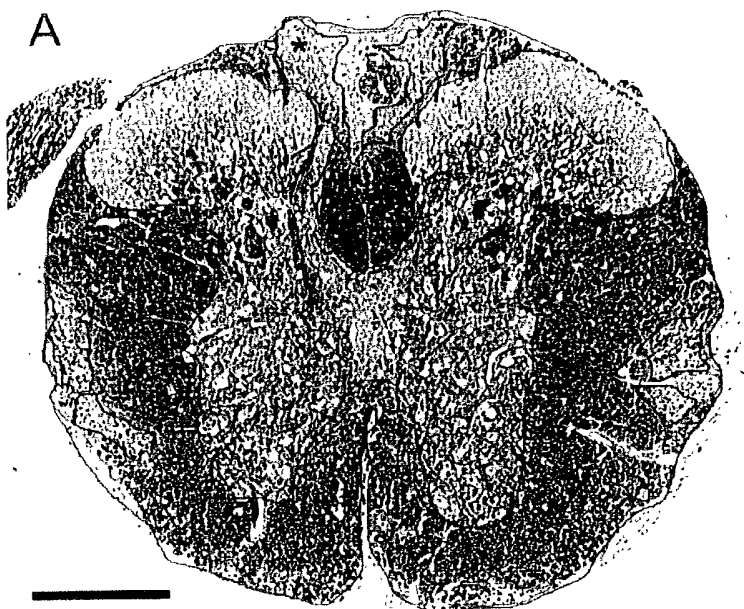
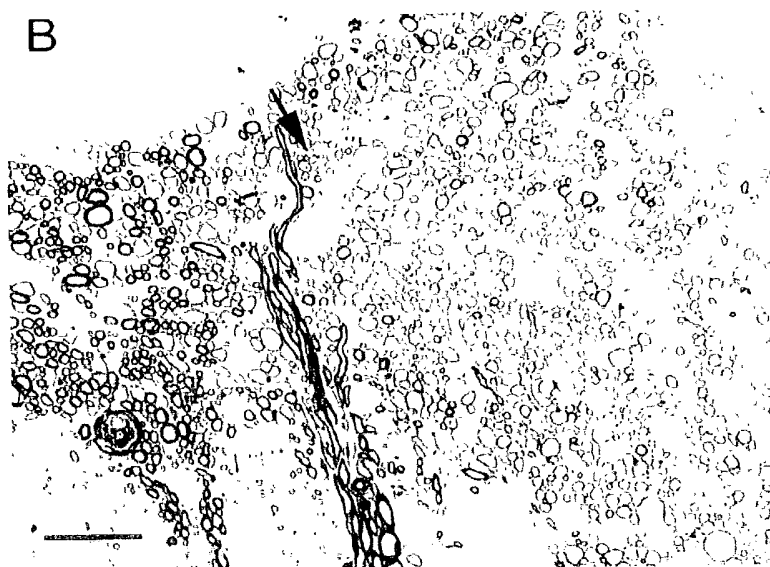


FIG. 42B



09/25/02
Jc685 U.S. PTO

FIG. 43A

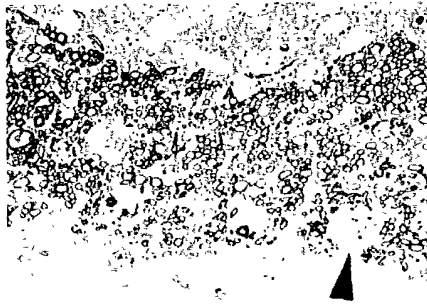


FIG. 43B

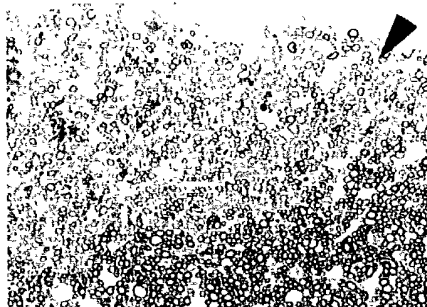


FIG. 43C

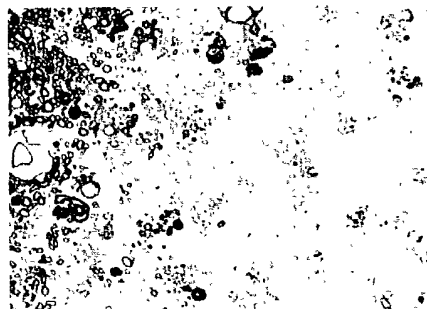


FIG. 43D

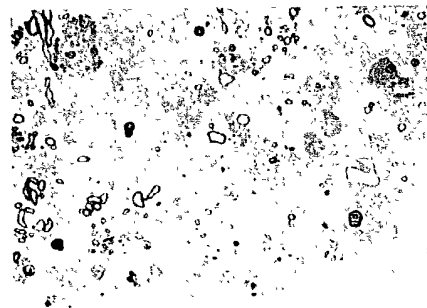


FIG. 43E

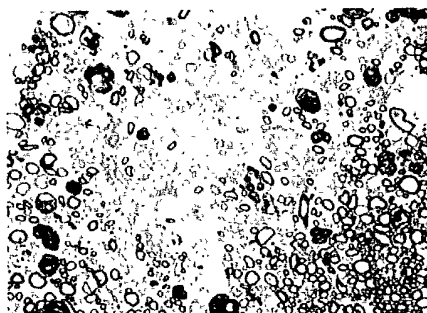


FIG. 43F

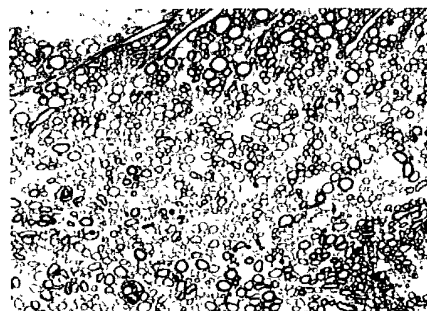


FIG. 43G



FIG. 43H

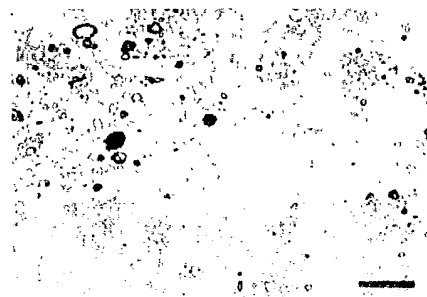


FIG. 44B

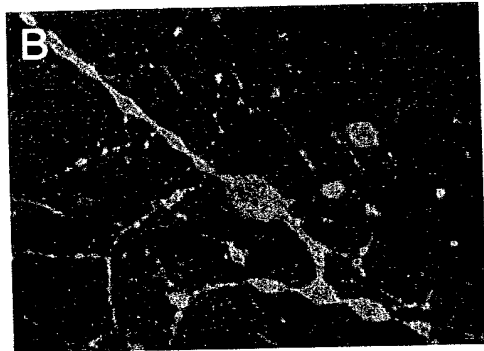


FIG. 44C

FIG. 44D



```

<----- F R 1 - I M G T -----
1          5          10          15          20
      x      A V V Q P G R S L R L S
      .AG . . . GCC GTG GTC CAG CCT GGG AGG TCC CTG AGA CTC TCC

----->
C A A S G F I F S S Y G M H W V R Q
TGT GCA GCG TCT GGA TTC ATT TTC AGT AGC TAT GGC . . . . . ATG CAC TGG GTC CGC CAG

----->
F R 2 - I M G T ----->
45 50 55 60 65
V P G K G L E W V A V I W Y D G S D K Y
GTT CCA GGC AAG GGG CTG GAG TGG GTG GCA GTT ATA TGG TAT GAT GGA AGT GAT AAA . . . TAC

----->
Y V D 70 S V K 75 R F T I S 80 D N S K 85 N T L Y
TAT GTA GAC TCC GTG AAG . . . GGC CGA TTC ACC ATC TCC AGA GAC AAT TCT AAA AAC ACG CTC TAT

----->
L Q M N S L 95 R A E D T 100 A V Y Y C 105 A R D R S 110 S
CTG CAA ATG AAC AGC CTG AGA GCC GAG GAC ACG GCT GTG TAT TAC TGT GCG AGA GAT CGC AGC AGT

CDR3 - IMGT
G W Y W S C D 115 S W G Q G 120 T L V I V 125 S S
GGC TGG TAC TGG TCC TGC GAC TCC TGG GGC CAG GGA ACC CTG GTC ATT GTC TCC TCA

```

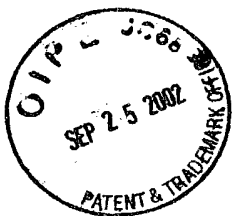


FIG. 46

Translation of CB2b-G8 V_λ

<----- F R 1 - I M G T ----->

1 5 10 15 20
... .TT XGC CTC ... CTG TCT GGG TCT CCT GGA CAG TCG ATC ACC ATC TCC

-----> CDR1 - IMGT <----->

25 30 35 40
C T G T S S D V G G Y N Y V S W Y Q Q
CTG ACT GGA ACC AGC AGT GAC GTT GGT GGT TAT AAC TAT ... GTC TCC TGG TAC CAA CAG

F R 2 - I M G T -----> CDR2 - IMGT <----->

45 50 55 60 65
H P G K A P K L M I Y D V S ... D
CAC CCA GGC AAA GCC CCC AAA CTC ATG ATT TAT GAT GTC AGT ... GAT

-----> F R 3 - I M G T ----->

70 75 80 85
R P S G V S N R F S G S K S G N T A S
CGG CCC TCA GGG GTT TCT ... AAT CGC TTC TCT GGC TCC AAG ... TCT GGC AAC ACG GCC TCC

-----> CDR3 - IMGT

90 95 100 105 110
L T I S G L Q A E D E A D Y Y C S S Y T S S
CTG ACC ATC TCT GGC CTC CAG GCT GAG GAC GAG GCT GAT TAT TAC TGC AGC TCA TAT ACA AGC AGC

115 120 125

130
S S V V F G G G T K L T V L G Q P K A A P S
AGC TCT GTG GTA TTC GGC GGA GGG ACC AAG CTG ACC GTC CTA GGT CAG CCC AAG GCT GCC CCC TCG

V T L F P P P x
GTC ACT CTG TTC CCG CCT CCA AXG G

FIG. 47A

DHFR amplification of 94.03k

4	5
0.2	51.2
51.2	0.2
0.2	51.2
Neg	Pos

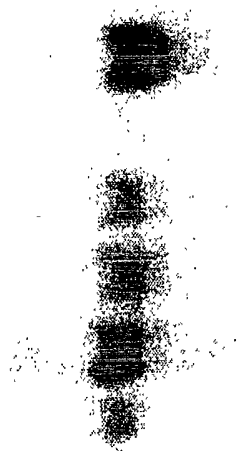


FIG. 47B

Clone #4 Kappa Chain Elisa

□ 0.2 ug/ml methotrexate
■ 51.2 ug/ml methotrexate

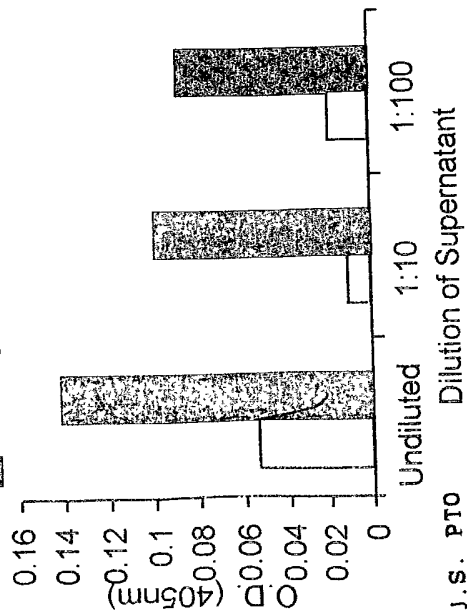


FIG. 47C

Clone #5 Kappa Chain Elisa

□ 0.2 ug/ml methotrexate
■ 51.2 ug/ml methotrexate

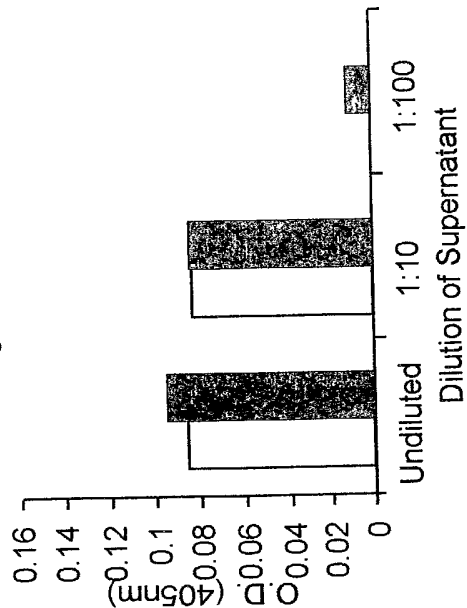
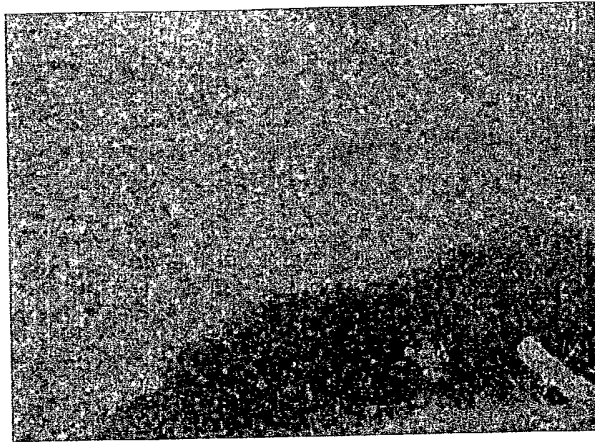
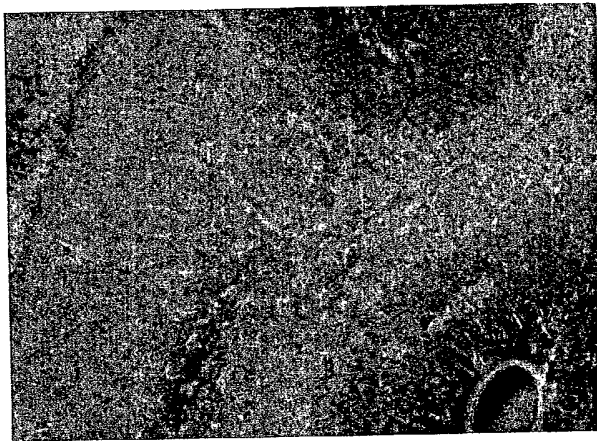


FIG. 49A



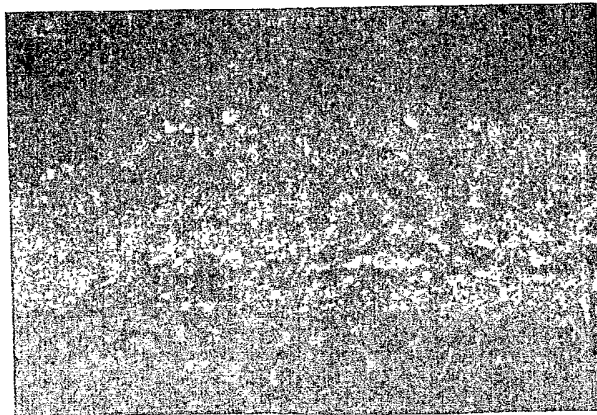
Mouse 94.03

FIG. 49B



Humanized 94.03
clone 1

FIG. 49C



Humanized 94.03
clone 2



FIG. 50A

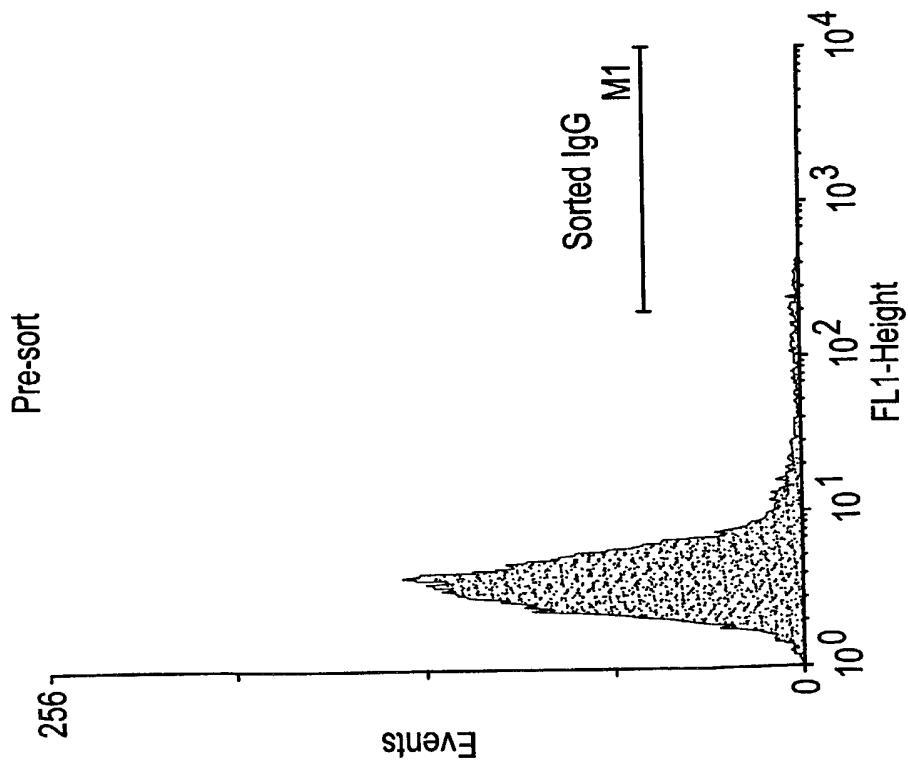


FIG. 50B

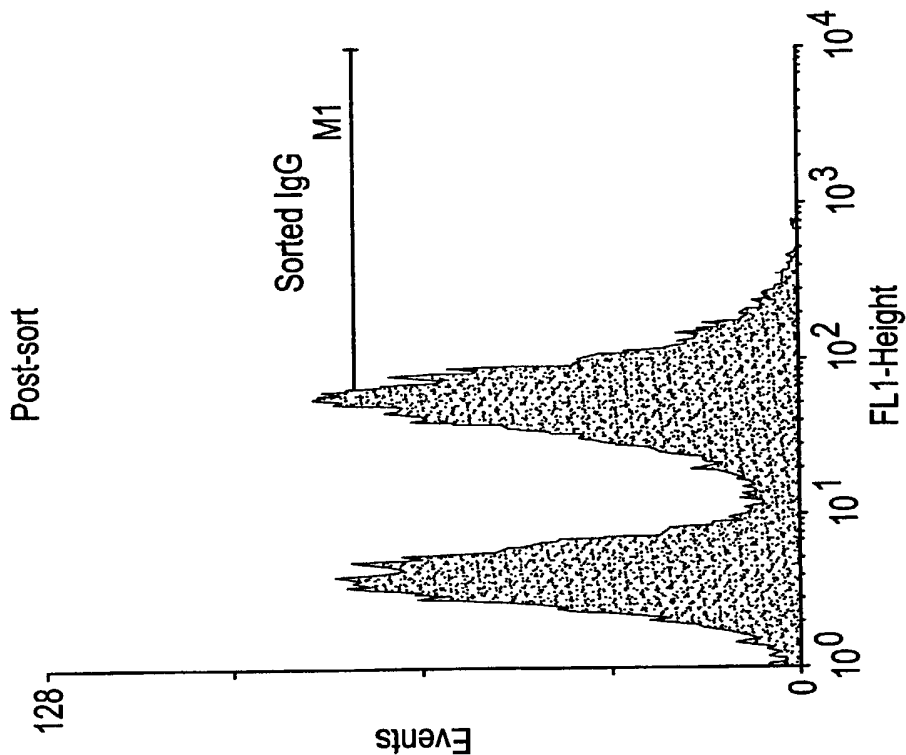
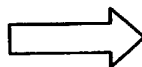
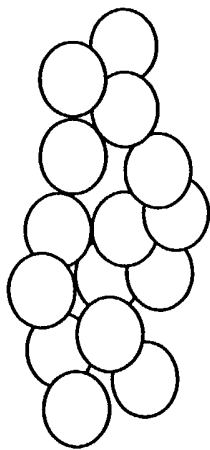




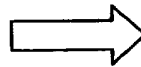
FIG. 51


Sequencing of 94.03 IgG

94.03 IgG Cloned Cells




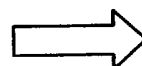
mRNA  AAAAAA



94.03 primer 

cDNA  TTTTTT

IgG1 primer 



PCR

ATGCAGTTACATGCATACTGAACTGCATGCTTTCCAG

Sequence with 94.03 V region plus IgG1

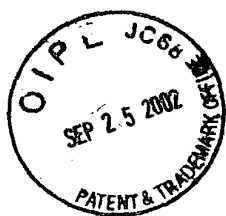


FIG. 52

09 V_H Sequence with translation:

<----- F R 1 - I M G T ----->

1 5 10 15 20
Q D H L Q Q S G P E L V K P G A F V K I S
CAG GAT CAC CTG CAG CAG TCT GGA CCT ...GAG CTG GTG AAG CCT GGG GCT TTT GTG AAG ATA TCC

-----> CDR1 - IMGT <----->

25 30 35 40
C K A S G Y T F T N Y D L N W V R Q
TGC AAG GCT TCT GGT TAC ACC TTC ACA AAC TAC GAT ...CTA AAC TGG GTG AGG CAG

F R 2 - I M G T -----> <--

45 50 55 60 65
R P G Q G L E W I G W I Y P G N D N T K
AGG CCT GGA CAG GGC CTT GAG TGG ATT GGA TGG ATT TAT CCT GGA AAT GAT AAT ACT ...AAG

-----> F R 3 - I M G T --

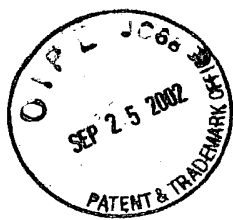
70 75 80 85
Y N E K F K G L A S L T A D K S S T T A Y
TAC AAT GAG AAG TTC AAG ...GGC CTG GCC TCA CTG ACT GCA GAC AAG TCC TCC ACC ACA GCC TAC

----->

90 95 100 105 110
L H L S S L T S E S S A V Y F C A R G L P R
TTG CAT CTC AGC AGC CTG ACT TCT GAG AGC TCT GCA GTC TAT TTC TGT GCA AGA GGG TTA CCT AGG

CDR3 - IMGT

115 120
G W Y F D V W G A G T T V T V S S A
GGC TGG TAC TTC GAT GTC TGG GGC GCA GGG ACC ACG GTC ACC GTC TCC TCA GCT



Translation of 09 kappa light chain 1:

FIG. 53

<----- F R 1 - I M G T ----->

1 5 10 15 20
N I V M T Q S P K S M S M S V G E R V T L T
AAC ATT GTA ATG ACC CAA TCT CCC AAA TCC ATG TCC ATG TCA GTA GGA GAG AGG GTC ACC TTG ACC

<----->

25 30 35 40
C K A S E N V V T Y V S W Y Q Q
TGC AAG GCC AGT GAG AAT GTG GTT ACT TAT ... GTT TCC TGG TAT CAA CAG

<----->

F R 2 - I M G T ----->

45 50 55 60 65
K P E Q S P K L L I Y G A S N
AAA CCA GAG CAG TCT CCT AAA CTG CTG ATA TAC GGG GCA TCC ... AAC

<----->

F R 3 - I M G T ----->

70 75 80 85
R Y T G V P D R F T G S G S A T D F T
CGG TAC ACT GGG GTC CCC ... GAT CGC TTC ACA GGC AGT GGA ... TCT GCA ACA GAT TTC ACT

<----->

90 95 100 105 110
L T I S S V Q A E D L A D Y H C G Q G Y S Y
CTG ACC ATC AGC AGT GTG CAG GCT GAA GAC CTT GCA GAT TAT CAC TGT GGA CAG GGT TAC AGC TAT

<----->

115
P Y T F G G
CCG TAC ACG TTC GGA GGG GGG

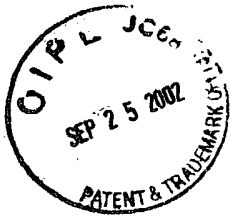


FIG. 54 Translation of 09 kappa light chain 2:

<----- F R I - I M G T ----->

1 5 10 15 20
D V Q I T Q S P S Y L A A F P G E T I T I N
GAT GTC CAG ATA ACC CAG TCT CCA TCT TAT CTT GCT GCA TTT CCT GGA GAA ACC ATT ACT ATT AAT

<----->

25 30 35 40
C R A S K S I S K Y L A W Y Q E
TGT AGG GCA AGT AAG AGC ATT AGT AAA TAT ... TTA GCC TGG TAT CAA GAG

<----->

F R 2 - I M G T ----->

45 50 55 60 65
R P G K T N K L L I Y S G S
AGA CCT GGA AAA ACT AAT AAG CTT ATC TAC TCT GGA TCC ... ACT

<----->

F R 3 - I M G T ----->

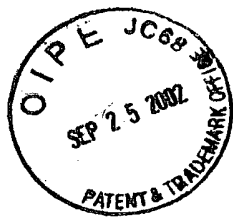
70 75 80 85
L Q S G I P S R F S G S G T D F T
TTG CAA TCT GGA ATT CCA ... TCA AGG TTC AGT GGC AGT GGA ... TCT GGT ACA GAT TTC ACT

<----->

90 95 100 105 110
L T I S S L E P E D F A M Y Y C Q Q H N E Y
CTC ACC ATC AGT AGC CTG GAG CCT GAA GAT TTT GCA ATG TAT TAC TGT CAA CAG CAT AAT GAA TAC

<----->

115
P Y T F G G
CCG TAT ACG TTC GGA GGG GGG



Translation of AKJR 4 Heavy Chain:

FIG. 55

<----- F R 1 - I M G T ----->

1 E V Q L L E S G G 10 G L V Q P G G S L R L S 20
GAG GTG CAA CTA TTG GAA TCT GGG GGA ... GGC TTG GTA CAG CCT GGG GGG TCC CTG AGA CTC TCC

<----->

CDR1 - IMGT 30 35 40
C A A S G F S F I D Y A M S W V R Q
TGT GCA GCC TCT GGA TTC AGC TTT ATC GAC TAT GCC ... ATG AGC TGG GTC CGC CAG

<----->

CDR2 - IMGT 55 60 65
F R 2 - I M G T -----> F R 3 - I M G T ----->

45 A P G G K G L E W V S S L S G D S G S S Y
GCT CCA GGG AAG GGA CTG GAG TGG GTC TCA AGT CTG AGT GGT GAT AGT GGT TCA ... TAT

<----->

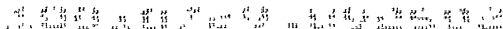
70 75 80 85
Y A D S V K G R F T I S R D N S K S T V F
TAT GCA GAC TCC GTG AAG ... GGC CGA TTC ACC ATC TCC AGA GAC AAT TCC AAG AGC ACG GTG TTT

<----->

CDR3 - IMGT 100 105 110
L Q L S S L R A E D T A I Y Y C A Q E T G P
CTG CAA CTG AGC AGC CTG AGA GCC GAG GAC ACG GCC ATA TAT TAC TGT GCG CAG GAG ACC GGT CCC

<----->

115 120 125 130
Q R R W G Q G T L V T V S S G S A S A P T L
CAG CGT CGC TGG GGC CAG GGA ACC CTG GTC ACC GTC TCC TCA GGG AGT GCA TCC GCC CCA ACC CTT



Translation of AKJR 4 Kappa Light Chain:

^



FIG. 57 Translation of CB2i-E12 Heavy Chain:

<----- F R 1 - I M G T ----->

1 5 10 15 20
x R x x x E A S V K V S
.CC AGG ... XAG XAX AXG AAA XCG GAG GCC TCA GTG AAG GTC TCC

<----->

CDR1 - IMGT 30 35 40
C K A S G Y T F T G Y Y M H W V R Q
TGC AAG GCT TCT GGA TAC ACC TTC ACC GGC TAC TAT ... ATG CAC TGG GTG CGA CAG

F R 2 - I M G T ----->

CDR2 - IMGT 55 60 65
A P G Q G L E W M G W I N P N S G G T N
GCC CCT GGA CAA GGG CTT GAG TGG ATG GGA TGG ATC AAC CCT AAC AGT GGT GGC ACA ... AAC

<----->

70 75 80 85
Y A Q K F Q G R V T M T R D T S I S T A Y
TAT GCA CAG AAG TTT CAG ... GGC AGG GTC ACC ATG ACC AGG GAC ACC TCC ATC AGC ACA GCC TAC

<----->

90 95 100 105 110
M E L S R L R S D D T A V Y Y C A R D R S Y
ATG GAG CTG AGC AGG CTG AGA TCT GAC GAC ACC GGC GTG TAT TAC TGT GCG AGA GAT CGA TCG TAT

CDR3 - IMGT 115 120 125
P G R N Y F D Y W G Q G T L V T
CCG GGA AGG AAC TAC TTT GAC TAC TGG GGC CAG GGA ACC CTG GTC ACC



FIG. 58 Translation of CB2i-E12 kappa chain:

<----- F R I - I M G T ----->

1 E I V L T Q S P G T L S L S P G E R A T L S
GAA ATT GTG TTG ACG CAG TCT CCA GGC ACC CTG TCT TCT CCA GGG GAA AGA GCC ACC CTC TCC

25 30 35 40
C R A S Q S V S S Y L A W Y Q Q
TGC AGG GCC AGT CAG AGT GTT AGC AGC AGC TAC ... TTA GCC TGG TAC CAG CAG

F R 2 - I M G T -----> CDR1 - IMGT CDR2 - IMGT
45 50 55 60 65
K P G Q A P R L L I Y G A S S
AAA CCT GGC CAG GCT CCC AGG CTC ATC TAT GGT GCA TCC ... AGC

70 75 80 85
R A T G I P D R F S S G S G T D F T
AGG GCC ACT GGC ATC CCA ... GAC AGG TTC AGT GGC AGT GGG ... TCT GGG ACA GAC TTC ACT

90 95 100 105 110
L T I S R L E P E D F A V Y Y C Q Q Y G S S
CTC ACC ATC AGC AGA CTG GAG CCT GAG GAA GAT TTT GCA GTG TAT TAC TGT CAG CAG TAT GGT AGC TCT

115
H T F G Q G
CAC ACT TTT GGC CAG GGG

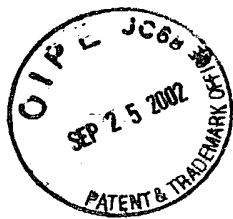


FIG. 59 Translation of CB2i-E7 Heavy Chain:

<----- F R 1 - I M G T ----->

1 5 10 15 20
x G L V K P G G S L R L S
... .GA ... GGC TTG GTC AAG CCT GGA GGG TCC CTG AGA CTC TCC

<----->

25 30 35 40
C A S G F T F S D Y Y M S W I R Q
TGT GCA GCC TCT GGA TTC ACC TTC AGT GAC TAC TACATG AGC TGG ATC CGC CAG

F R 2 - I M G T ----->

45 50 55 60 65
A P G K G L E W V S Y I S S S Y T N
GCT CCA GGG AAG GGG CTG GAG TGG GTT TCA TAC ATT AGT AGT AGT AGT TAC ACAAAC

<----->

70 75 80 85
Y A D S V K G R F T I S R D N A K N S L Y
TAC GCA GAC TCT GTG AAG ... GGC CGA TTC ACC ATC TCC AGA GAC AAC GCC AAG AAC TCA CTG TAT

<----->

90 95 100 105 110
L Q M N S L R A E D T A V Y Y C A R D R S S
CTG CAA ATG AAC AGC CTG AGA GCC GAG GAC ACC GCT GTG TAT TAC TGT GCG AGA GAT CGG TCG AGC

CDR3 - IMGT

115 120 125
S S W Y Y Y Y G M D V W G Q G
AGC AGC TGG TAC TAC TAC TAC TAC GGT ATG GAC GTC TGG GGC CAA GGG



FIG. 60 Translation of CB2i-E7 kappa Chain:

----- F R 1 - I M G T -----

1 D I Q M T Q S P S L S A S V G D R V T I T 20
GAC ATC CAG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA GAC AGA GTC ACC ATC ACT

-----> <-----

25 30 35 40
C R A S Q G I S N Y L A W Y Q Q
TGC CGG GCG AGT CAG GGC ATT AGC AAT TAT ... TTA GCC TGG TAT CAG CAG

F R 2 - I M G T -----> <-----

45 50 55 60 65
K P G K V P K L I Y A A S T
AAA CCA GGG AAA GTT CCT AAG CTC CTG ATC TAT GCT GCA TCC ... ACT

----- F R 3 - I M G T -----

70 75 80 85
L Q S G V P S R F N G S G S G T D F T
TTG CAA TCA GGG GTC CCA ... TCT CGG TTC AAT GGC AGT GGA ... TCT GGG ACA GAT TTC ACT

-----> <-----

90 95 100 105 110
L T I S S L Q P E D V A T Y Y C Q K Y N K C
CTC ACC ATC AGC AGC CTG CAA CCT GAA GAT GTT GCA ACT TAT TAC TGT CAA AAG TAT AAC AAG TGC

-----> <-----

115
P S H F R G R D
CCC TCT CAC TTT CGG GGG AGG GAC



FIG. 61

Translation Of MSI 19-E5 Light Chain

```
<----- F R 1 - I M G T ----->
      5      10      15      20
1  D I A M T Q S P D S L A V S L G E R A T I N
   GAC ATC GCG ATG ACC CAG TCT CCA GAC TCC CTG GCA GTG TCT CTG GGC GAG AGG GCC ACC ATC AAC

<----->
      30      35      40
25 C K S S R S V L F S S N N N Y L A W Y Q Q
    TGC AAG TCC AGC CGG AGT GTT TTA TTC AGC TCC AAC AAT AAC TAC TTA GCT TGG TAC CAG CAG

F R 2 - I M G T ----->
      50      55      60      65
45 K P G Q P P K L L I Y W A S
    AAA CCA GGA CAG CCT CCT AAG CTA CTC ATT TAC TGG GCA TCT ... ACC
                                     CDR2 - IMGT
                                     60      65
                                     T

F R 3 - I M G T ----->
      70      75      80      85
R E S G V P D R F S G S G S G T D F T
CGG GAA TCC GGG GTC CCT ... GAC CGA TTC AGT GGC AGC GGG ... TCT GGG ACA GAT TTC ACT

<----->
      90      95      100      105      110
L T I S S L Q A E D V A V Y Y C Q Q Y Y S T
CTC ACC ATC AGC AGC CTG CAG GCT GAA GAT GTG GCA GTT TAT TAC TGT CAG CAA TAT TAT AGT ACT

MGF
P I T F G
CCA ATC ACC TTC GGC
```



Translation of 04 kappa chain 2:

FIG. 62

<----- F R 1 - I M G T ----->

1 5 10 15 20
D I V M T Q S H K F M S T S V G D R V S I T
GAC ATC GTA ATG ACG CAG TCT CAC AAA TTC ATG TCC ACT TCA GTA GGA GAC AGG GTC AGC ATC ACC

<----->

25 30 35 40
C K A S Q D V S T A V A W Y Q Q
TGC AAG GCC AGT CAG GAT GTG AGT ACT GCT GTA GCC TGG TAT CAA CAG

F R 2 - I M G T ----->

45 50 55 60
K P G Q S P K L L I Y S A S Y
AAA CCA GGA CAA TCT CCT AAA CTA CTG ATT TAC TCG GCA TCC TAC

<----->

70 75 80 85
R Y T G V P D R F T G S G S G T D F T
CGG TAC ACT GGA GTC CCT ... GAT CGC TTC ACT GGC AGT GGA TCT GGG ACG GAT TTC ACT

<----->

90 95 100 105 110
F T I S S V Q A E D L A V Y Y C Q Q H Y T T
TTC ACC ATC AGC AGT GTG CAG GCT GAA GAC CTG GCA GTT TAT TAC TGT CAG CAA CAT TAT ACT ACT

115
P L T F G A G
CCG CTC ACG TTC GGT GCT GGG



FIG. 63A

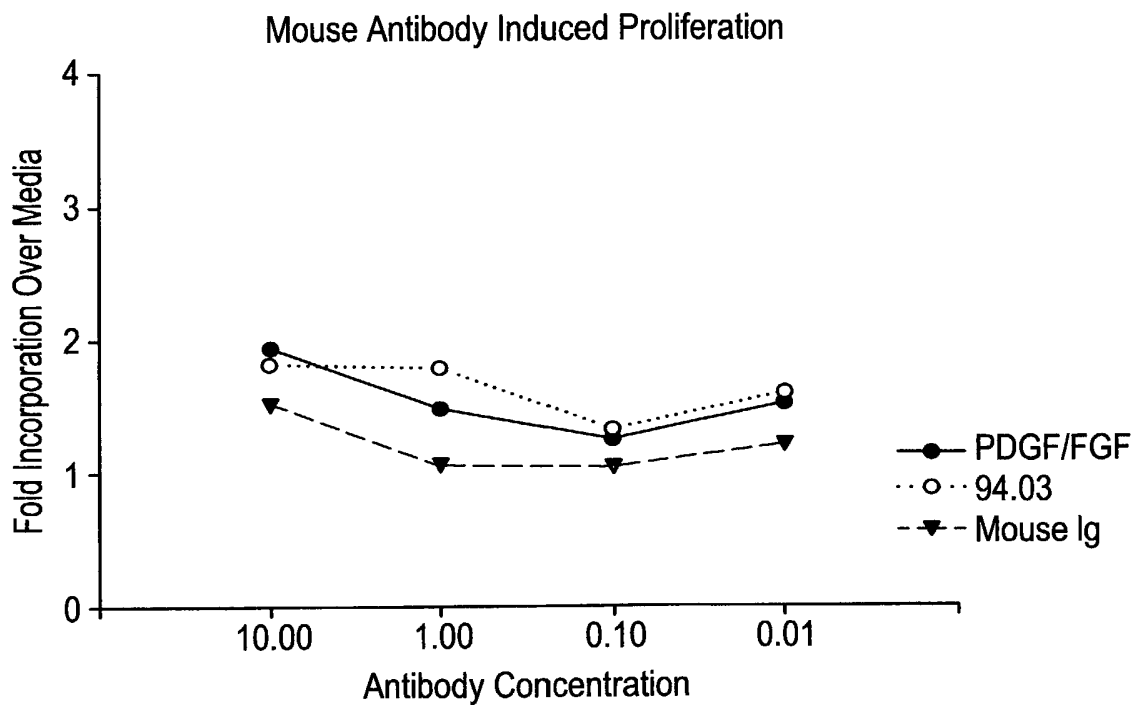


FIG. 63B

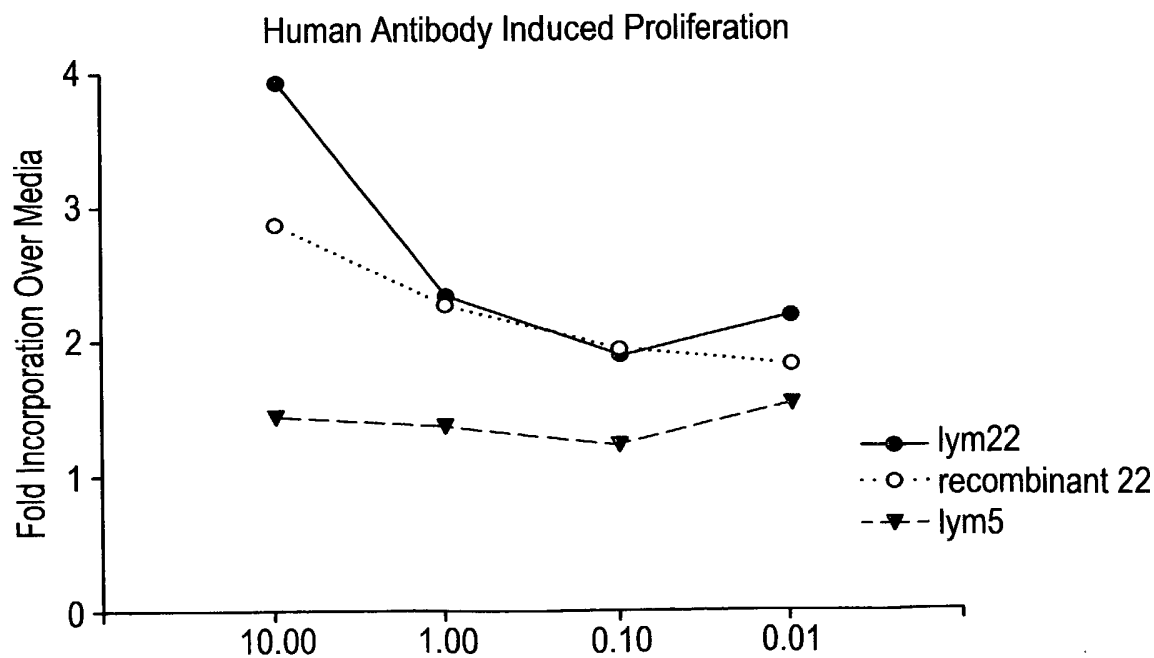
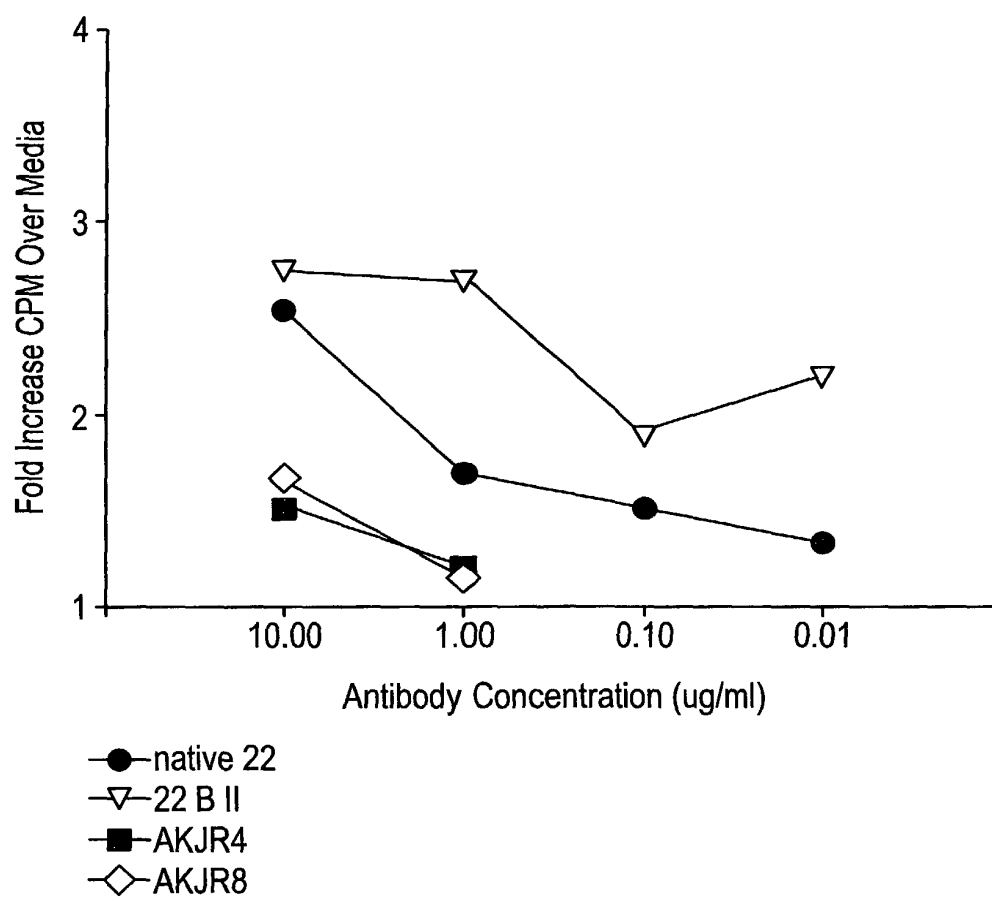
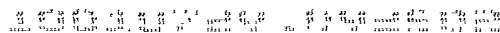




FIG. 64

Human Antibody Induced 3H Thymidine Incorporation





Mouse Antibody Induced 3H Thymidine Incorporation

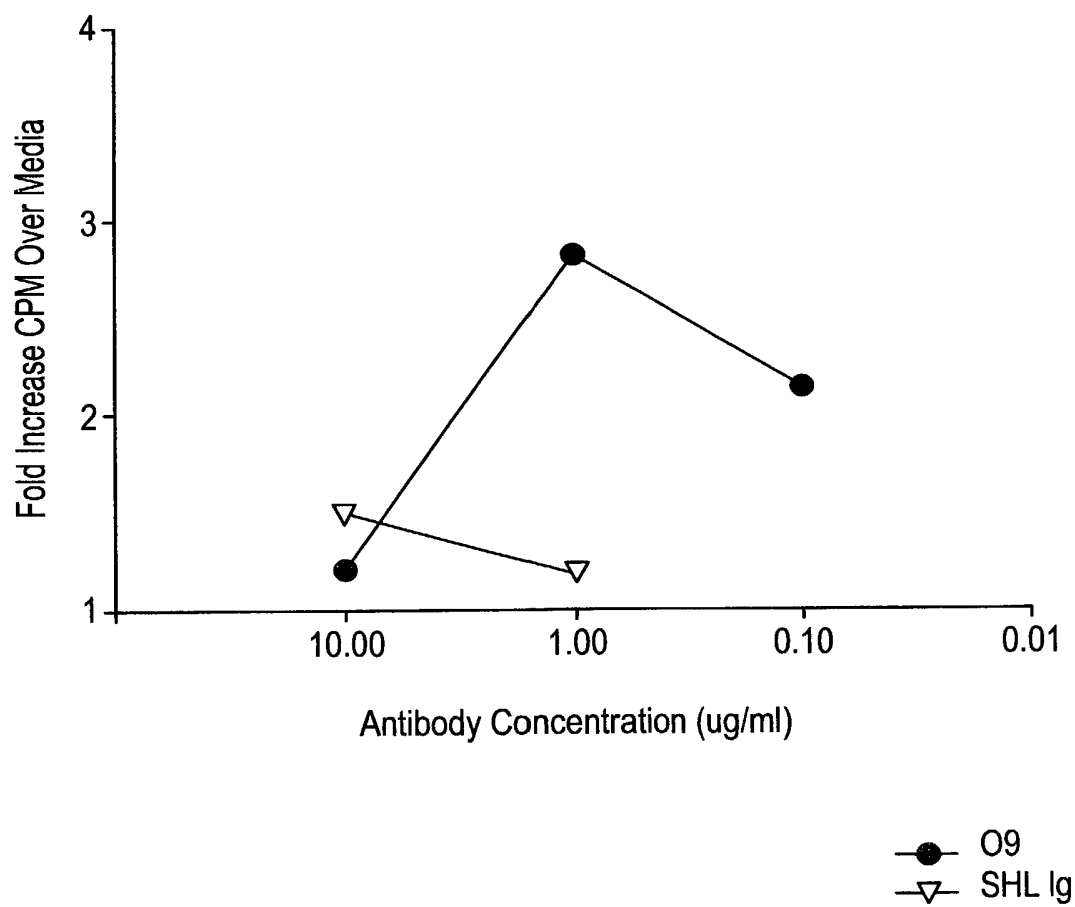
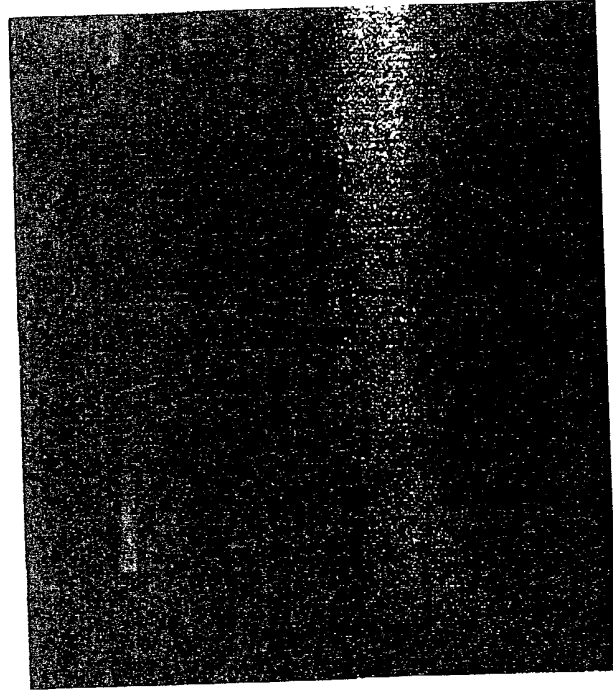
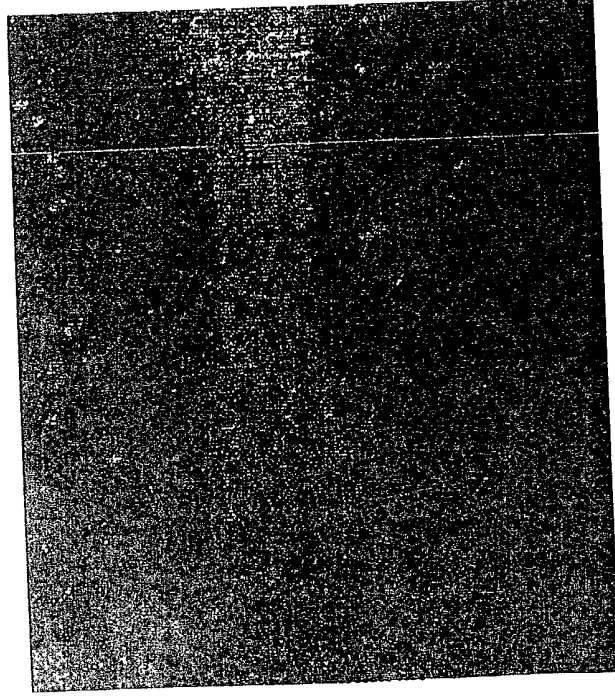


FIG. 66B



rHlgM 22

FIG. 66A



sHlgM 22

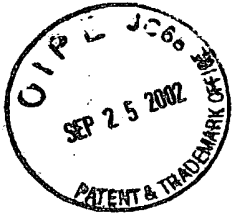


FIG. 69 TRANSLATION OF HNK-1 KAPPA CHAIN

<----- F R I - I M G T ----->

1 5 10 15 20
D I Q M T Q S P S L S A S L G E R V S L T
GAC ATC CAG ATG ACC CAG TCT CCA TCC TCC TTA TCT GCC TCT CTG GGA GAA AGA GTC AGT CTC ACT

<----->

25 30 35 40
C R A S Q D I G S S L N W L Q Q
TGT CGG GCA AGT CAG GAC ATT GGT AGT AGC ... TTA AAC TGG CTT CAG CAG

F R 2 - I M G T -----> CDR1 - IMGT CDR2 - IMGT <----->

45 50 55 60 65
E P D G T I K R L I Y A T S
GAA CCA GAT GGA ACT ATT AAA CGC CTG ATC TAC GCC ACA TCC ... AGT

----- F R 3 - I M G T ----->

70 75 80 85
L D S G V P K R F S G S R S G S D Y S
TTA GAT TCT GGT GTG CCC ... AAA AGG TTC AGT GGC AGT AGG ... TCT GGG TCA GAT TAT TCT

<----->

90 95 100 105 110
L T I S S L E S E D F V D Y Y C L Q Y A S
CTC ACC ATC AGC AGC CTT GAG TCT GAA GAT TTT GTA GAC TAT TAC TGT CTA CAA TAT GCT AGT TTT

----->

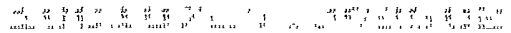
115
P Y T F G G G T K L E I K R
CCG TAC ACG TTC GGA GGG GGG ACC AAG CTG GAA ATA AAA CGG



FIG. 70

TRANSLATION OF A2B5 KAPPA CHAIN

1 Q I V L T Q S P A I M S A S P G E K V T I S
CAA ATT GTT CTC ACC CAG TCT CCA GCA ATC ATG TCT GCA TCT CCA GGG GAG AAG GTC ACC ATA TCC
20
25 C S A S S S V S Y 30 CDR1 - IMGT 35 40 M Y W Y Q Q
TGC AGT GCC AGC TCA AGT GTA AGT TAC ATG TAC TGG TAC CAG CAG
F R 2 - I M G T -----> CDR2 - IMGT 60 65 N
45 K P G S S P K P W I Y R T S
AAG CCA GGA TCC TCC CCC AAA CCC TGG ATT TAT CGC ACA TCC AAC
F R 3 - I M G T ----->
70 L A S G V P A R F S G S G 80 S G T S Y S
CTG GCT TCT GGA GTC CCT ... GCT CGC TTC AGT GGC AGT GGG ... TCT GGG ACC TCT TAC TCT
90 L T I S S M E A E D A A T Y Y C Q Q Y H S Y
CTC ACA ATC AGC AGC ATG GAG GCT GAA GAT GCT GCC ACT TAT TAC TGC CAG CAG TAT CAT AGT TAC
100
110 CDR3 - IMGT
115 P L T F G A G T K L E L K R
CCA CTC ACG TTC GGT GCT GGG ACC AAG CTG GAG CTG AAA CGG



LYM 46 Heavy Chain Sequence:

FR 1														
E	V	Q	L	V	E	S	G	G	G	L	V	Q	P	G
GAG	GTG	CAG	CTG	GTG	GAG	TCT	GGG	GGA	GGC	TTG	GTC	CAG	CCT	GGG
CDR1														
G	S	L	R	L	S	C	A	A	S	G	F	T	F	S
GGG	TCC	CTG	AGA	CTC	TCC	TGT	GCA	GCC	TCT	GGA	TTC	ACC	TTT	AGT
FR 2														
S	Y	W	M	T	W	V	R	Q	A	P	G	K	G	L
AGC	TAT	TGG	ATG	ACC	TGG	GTC	CGC	CAG	GCT	CCA	GGG	AAG	GGG	CTG
CDR2														
E	W	V	A	N	I	K	K	D	G	S	E	K	S	Y
GAG	TGG	GTG	GCC	AAC	ATA	AAG	AAA	GAT	GGA	AGT	GAG	AAA	TCC	TAT
FR3														
V	D	S	V	K	G	R	F	T	T	S	R	D	N	A
GTG	GAC	TCT	GTG	AAG	GGC	CGA	TTC	ACC	ACC	TCC	AGA	GAC	AAC	GCC
CDR3														
K	N	S	L	Y	L	Q	M	N	S	L	R	A	E	D
AAG	AAC	TCA	CTG	TAT	CTG	CAA	ATG	AAC	AGC	CTG	AGA	GCC	GAG	GAC
CDR3														
T	A	V	Y	Y	C	A	R	P	N	C	G	G	D	C
ACG	GCT	GTG	TAT	TAC	TGT	GCG	AGA	CCC	AAT	TGT	GGT	GGT	GAC	TGC
CDR3														
Y	L	P	W	Y	F	D	L	W	G	R	G	T	L	V
TAT	TTA	CCA	TGG	TAC	TTC	GAT	CTC	TGG	GGC	CGT	GGC	ACC	CTG	GTC
CDR3														
T	V	S	S											
ACT	GTC	TCC	TCA											

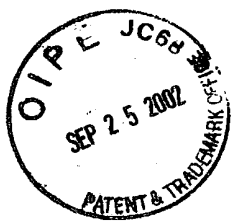


FIG. 72

YM 46 KAPPA LIGHT CHAIN SEQUENCE:

----- F R I - I M G T -----

5 10 15 20
D I V M T Q S P D S L A V S L G E R A T I N
AC ATC GTG ATG ACC CAG TCT CCA GAC TCC CTG GCT GTG TCT CTG GGC GAG AGG GCC ACC ATC AAC

-----> <-----

CDR1 - IMGT 30 35 40
C K S S Q S V L Y S S N N K N Y L A W Y Q Q
GC AAG TCC AGC CAG AGT GTT TTA TAC AGC TCC AAC AAT AAG AAC TAC TTA GCT TGG TAC CAG CAG

-----> <-----

CDR2 - IMGT 55 60 65
R 2 - I M G T ----- F R 3 - I M G T -----

5 50 55 60 65
K P G Q P P K L L I Y W A S
AA CCA GGA CAG CCT CCT AAA CTA CTC ATT TAC TGG GCA TCT ACC

-----> <-----

70 75 80 85
R E S G V P D R F S G S G T D F T
GG GAA TCC GGG GTC CCT ... GAC CGA TTC AGT GGC AGC GGG ... TCT GGG ACA GAT TTC ACT

-----> <-----

CDR3 - IMGT 100 105 110
L T I S S L Q A E D V A V Y Y C Q Q Y Y N T
TC ACC ATC AGC AGC CTG CAG GCT GAA GAT GTG GCA GTT TAT TAC TGT CAG CAA TAT TAT AAT ACT

-----> <-----

115 120 125 130
P Q A F G Q G T K V E I K R T V A A P S V F
CT CAG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA CGA ACT GTG GCT GCA CCA TCT GTC TTC

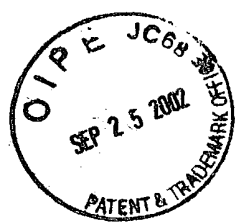


FIG. 73

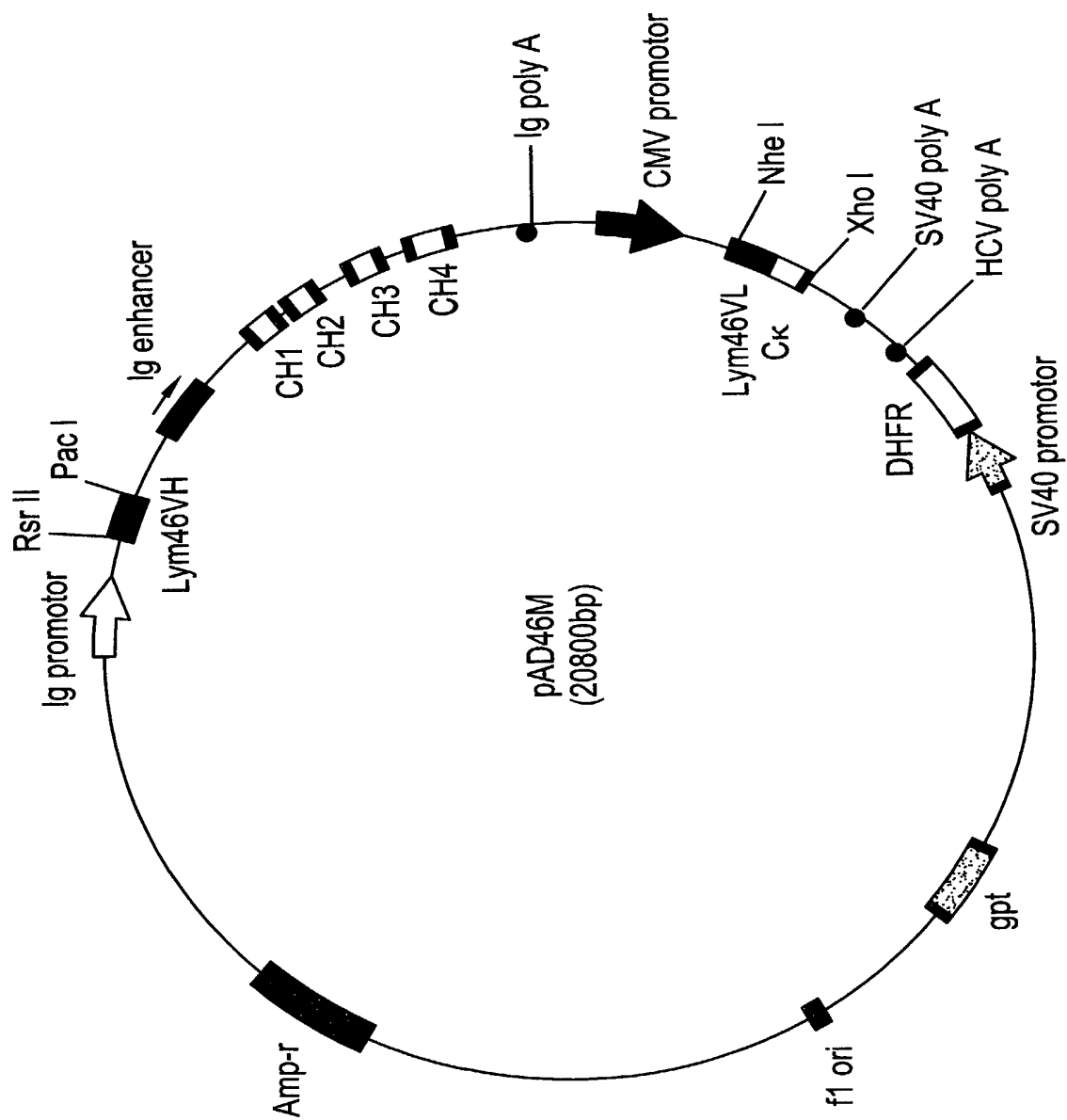
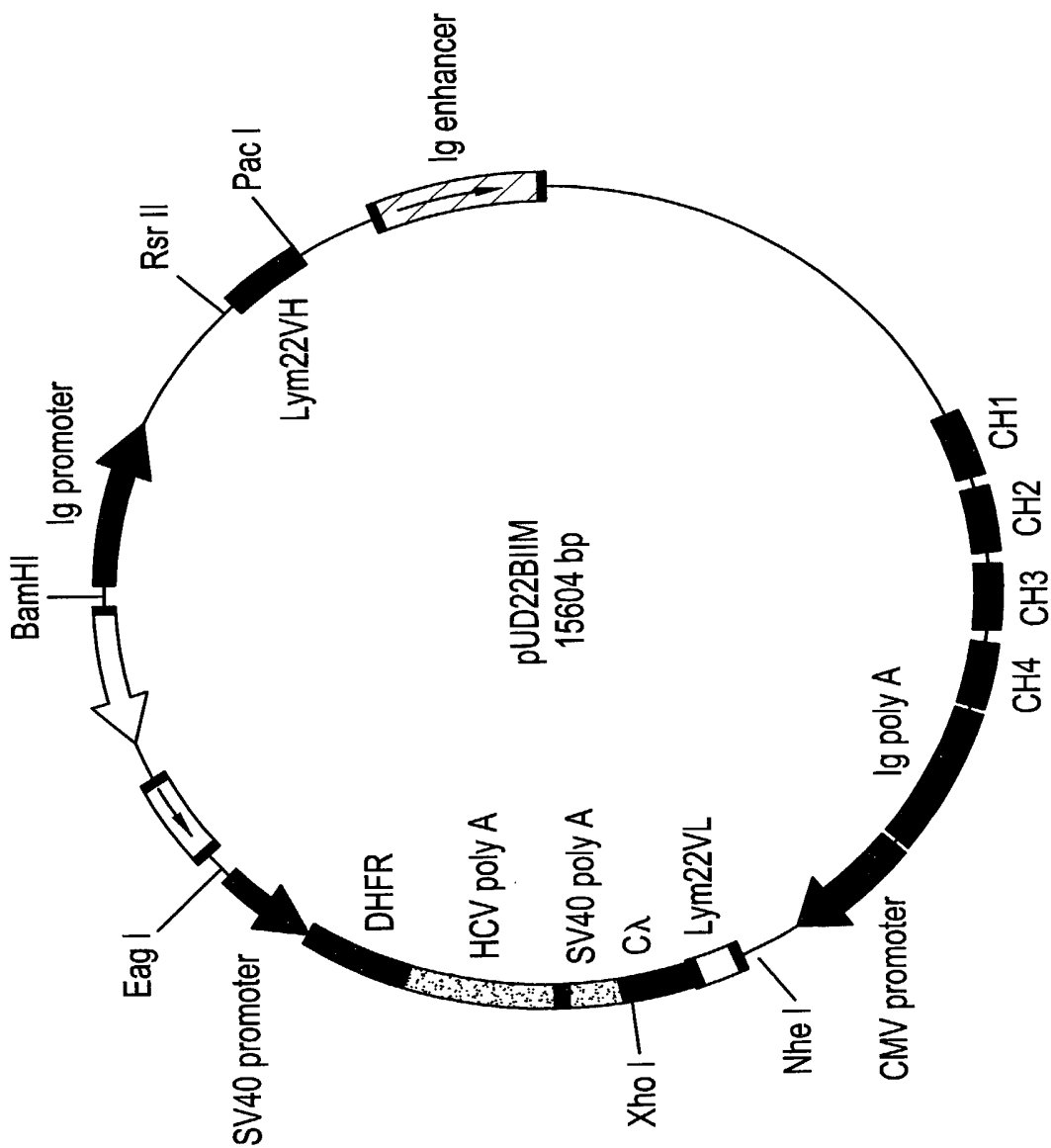




FIG. 74



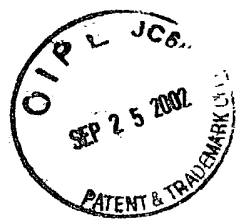


FIG. 75

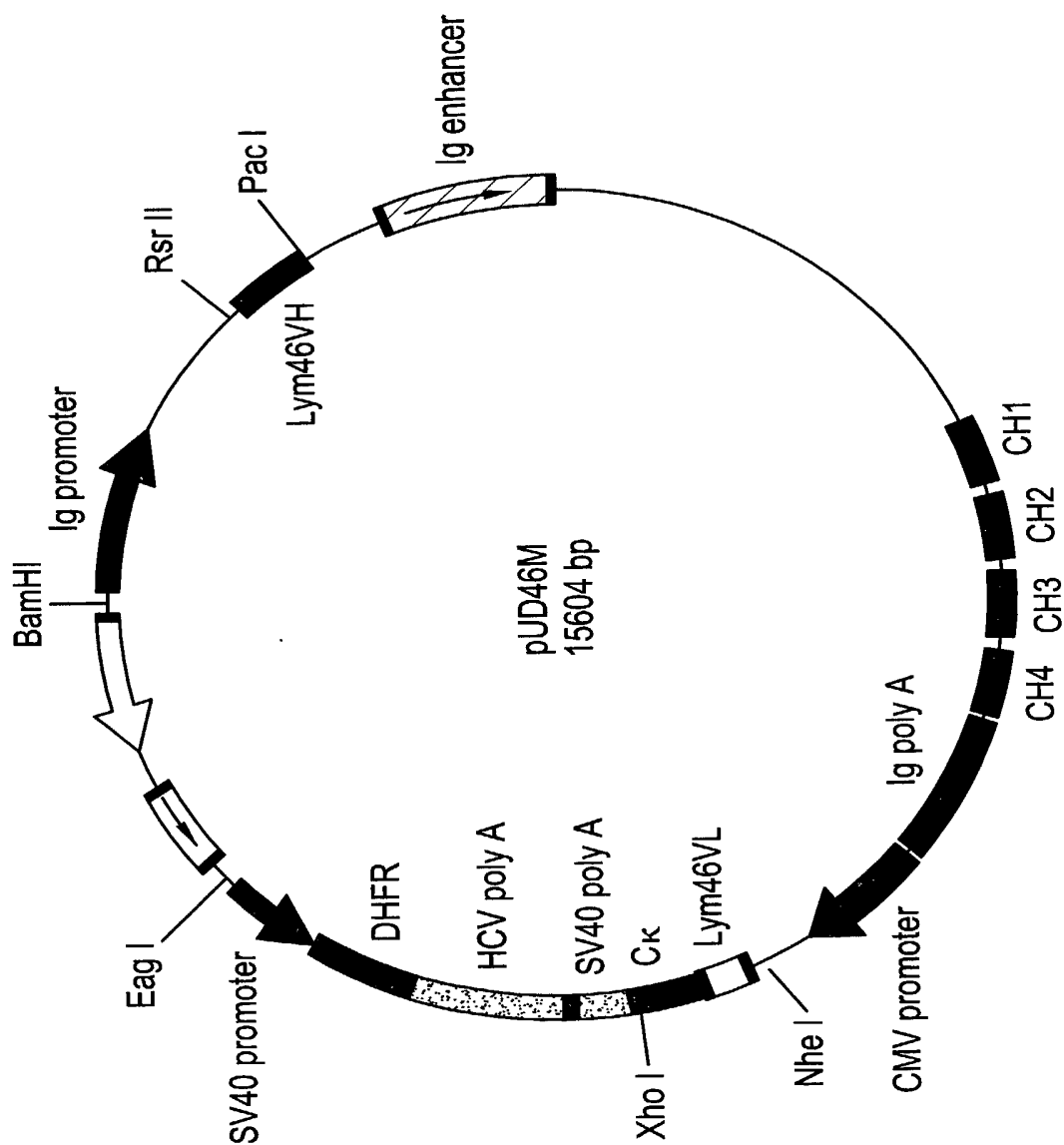




FIG. 76

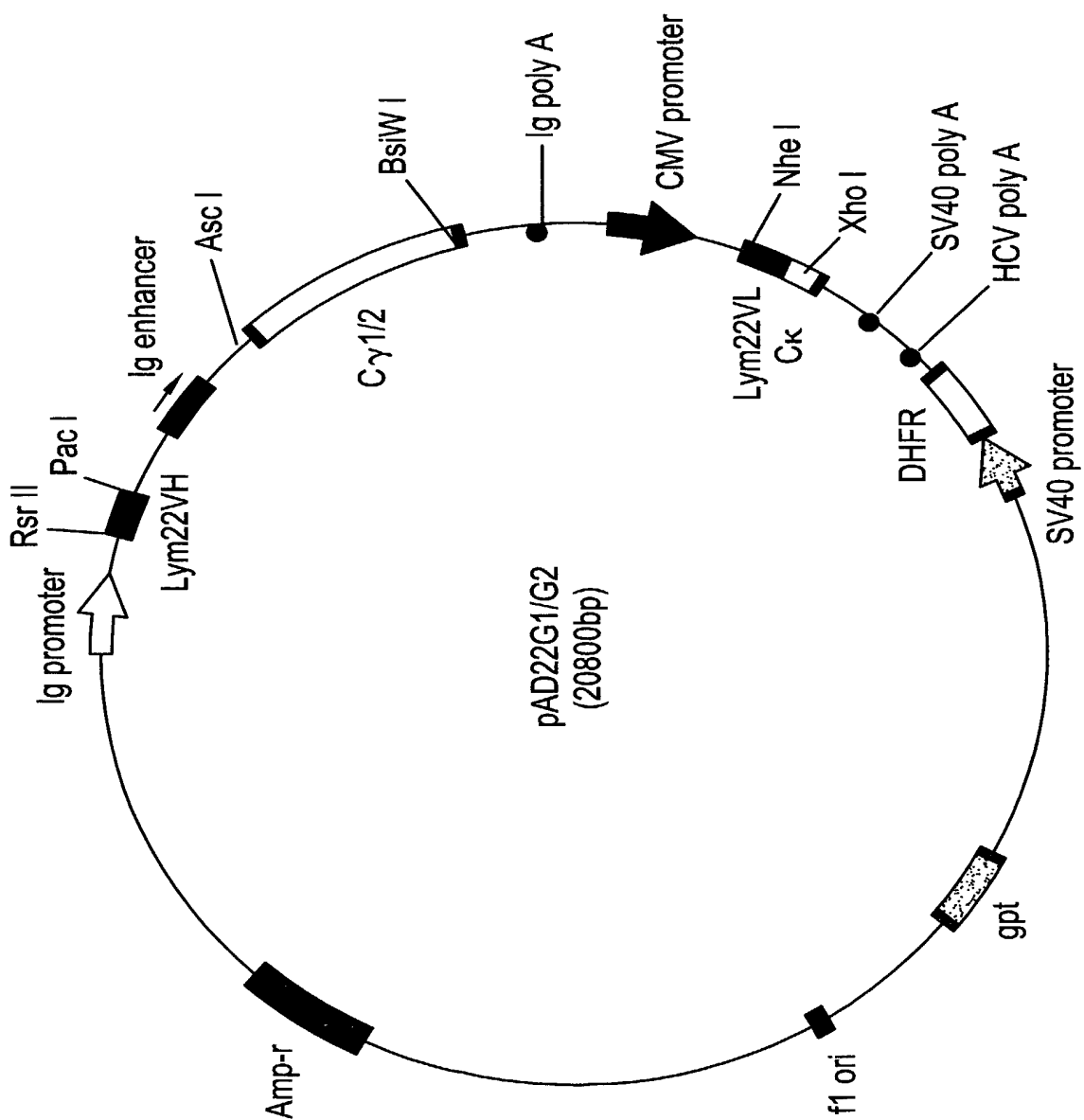




FIG. 77

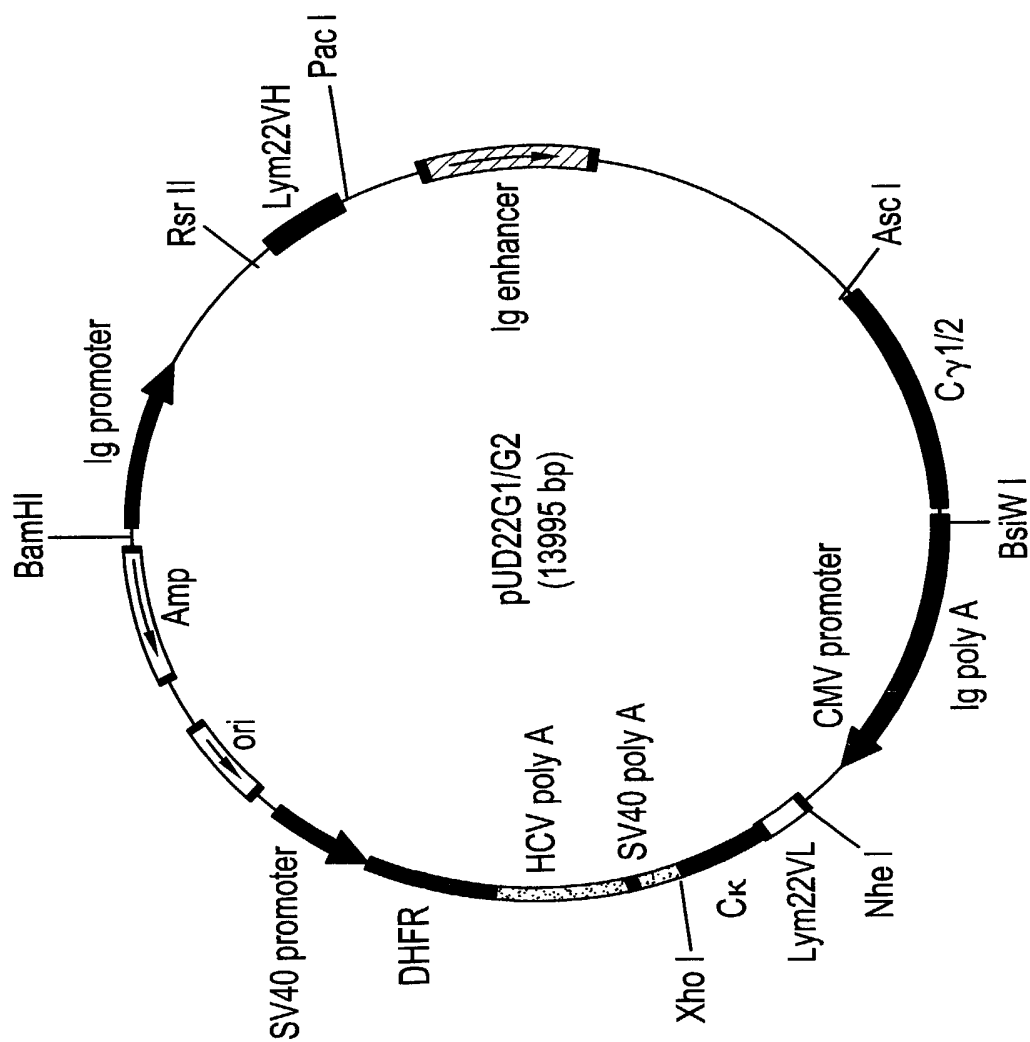
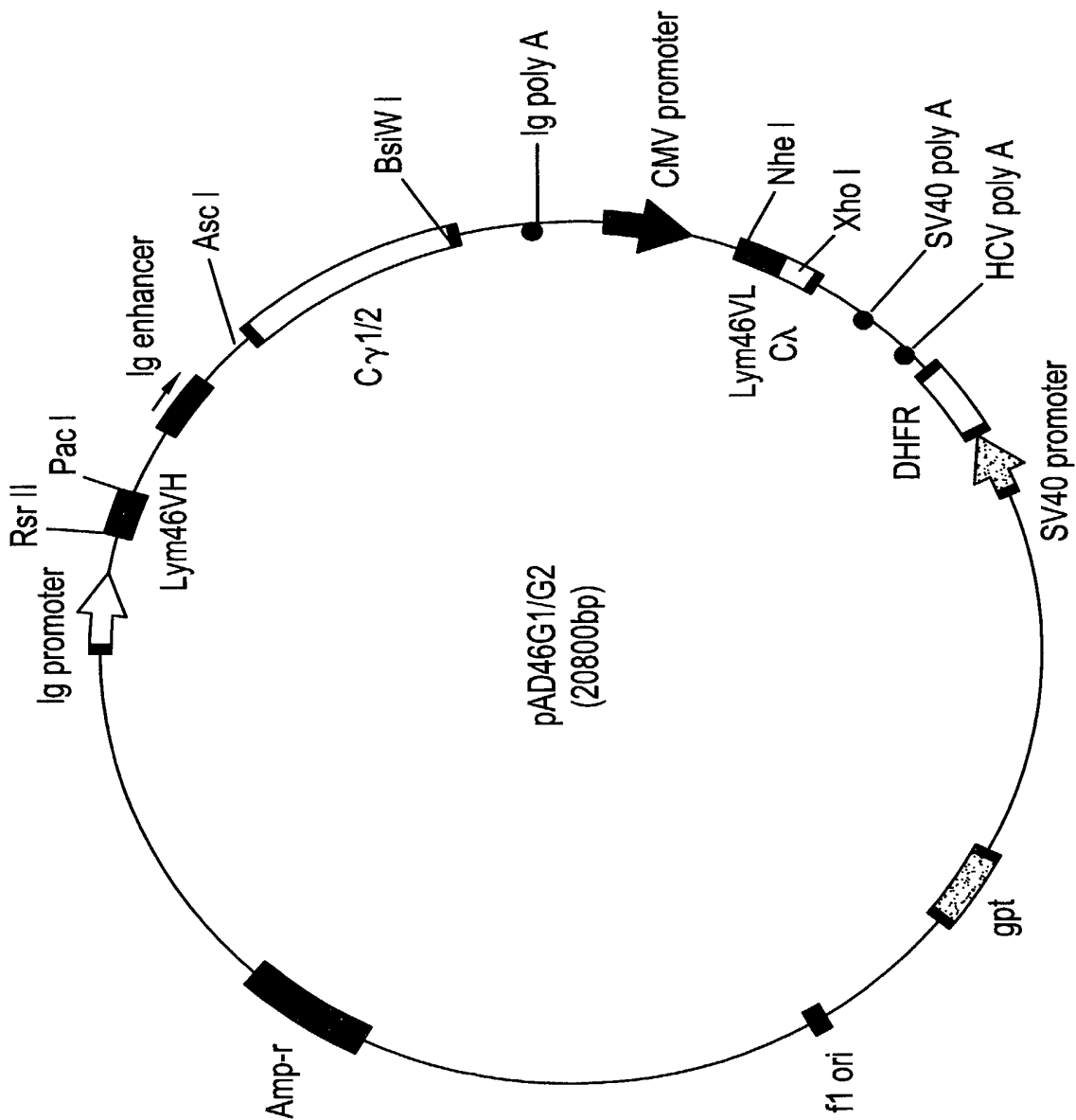




FIG. 78



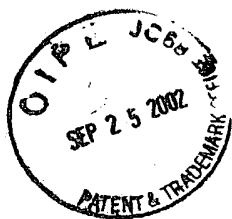


FIG. 79

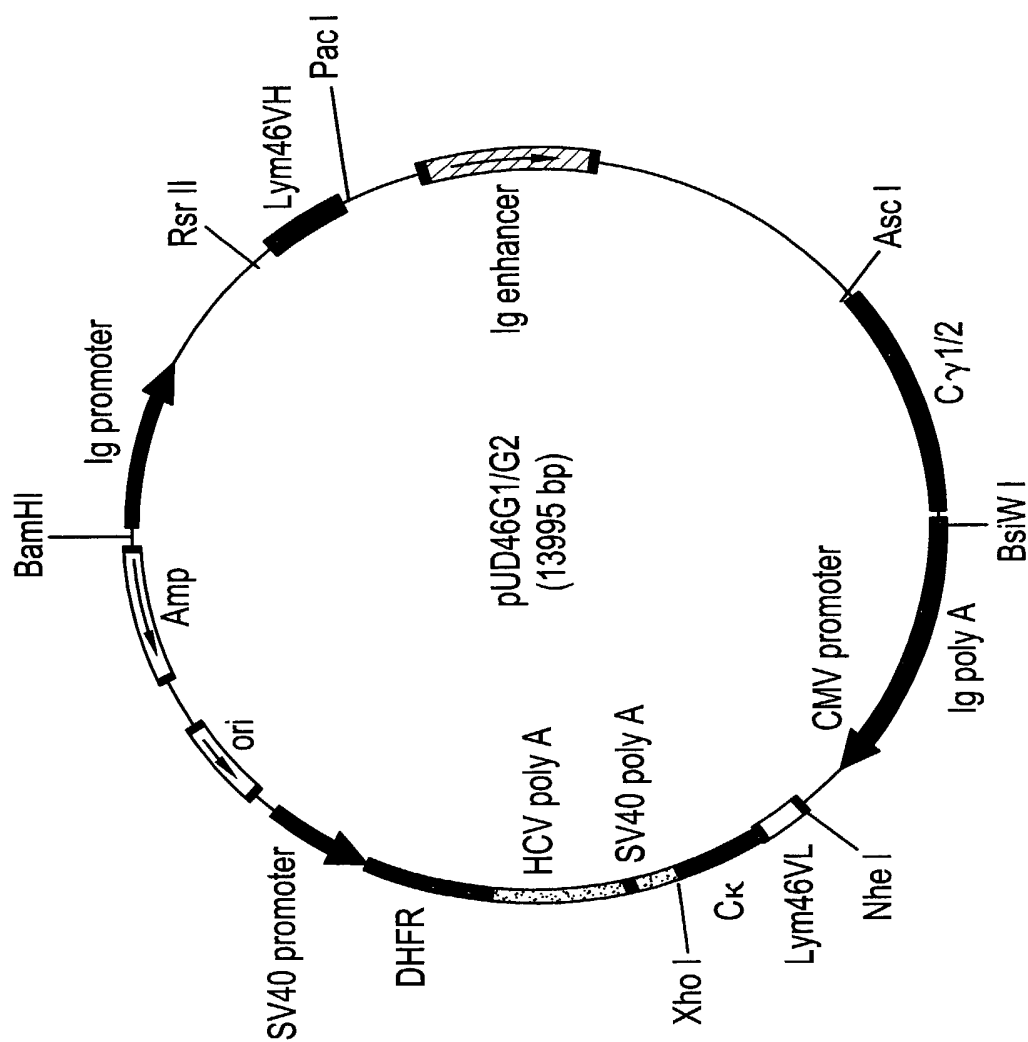




FIG. 80A

TMEV Infected SJL Mice
Treated at 21 Days Post Infection

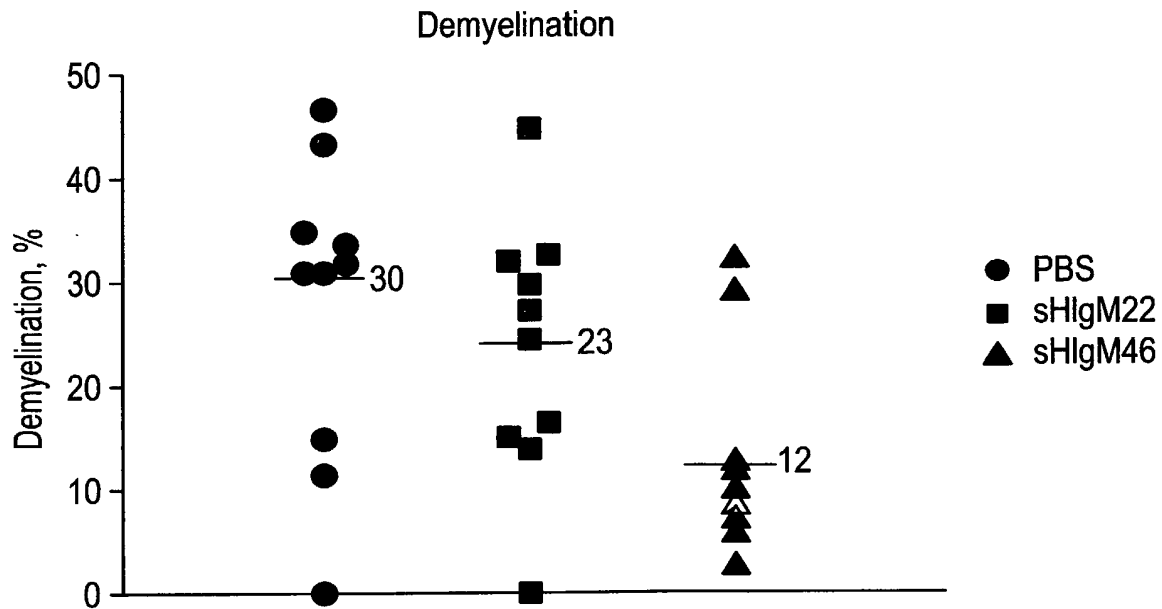
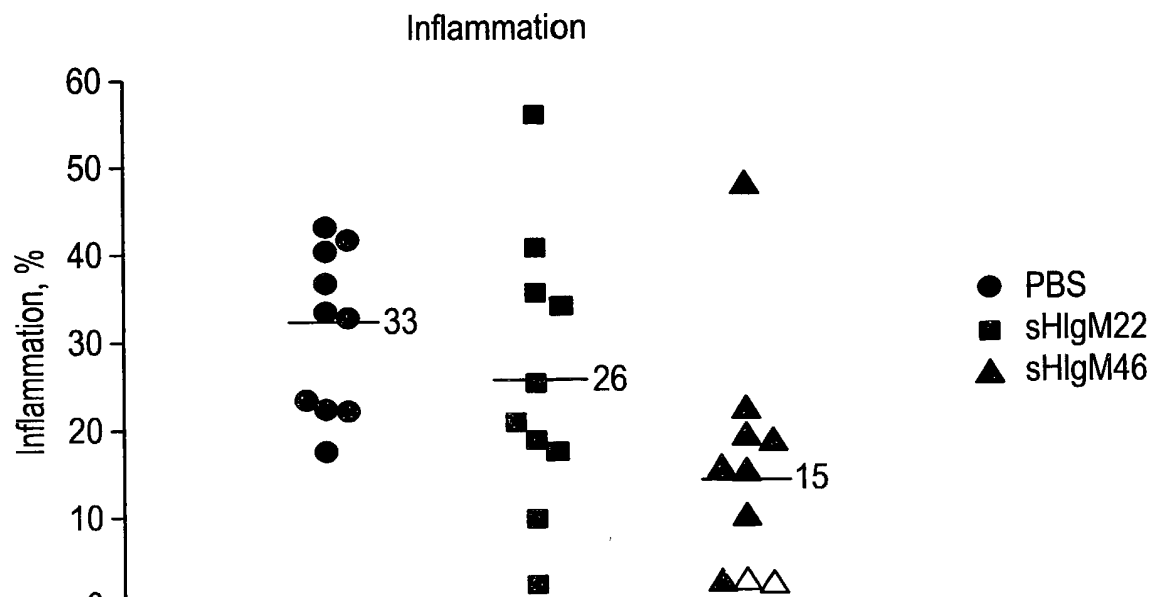
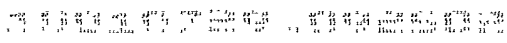


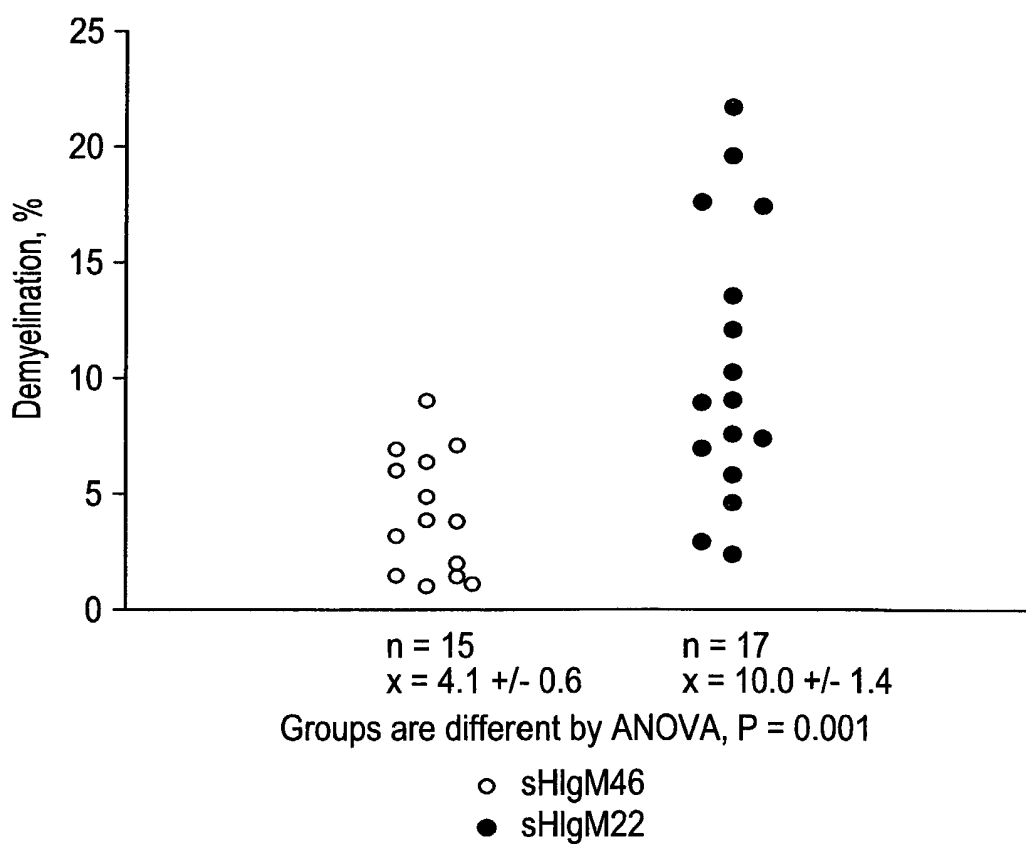
FIG. 80B

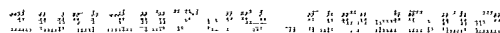
TMEV Infected SJL Mice
Treated at 21 Days Post Infection



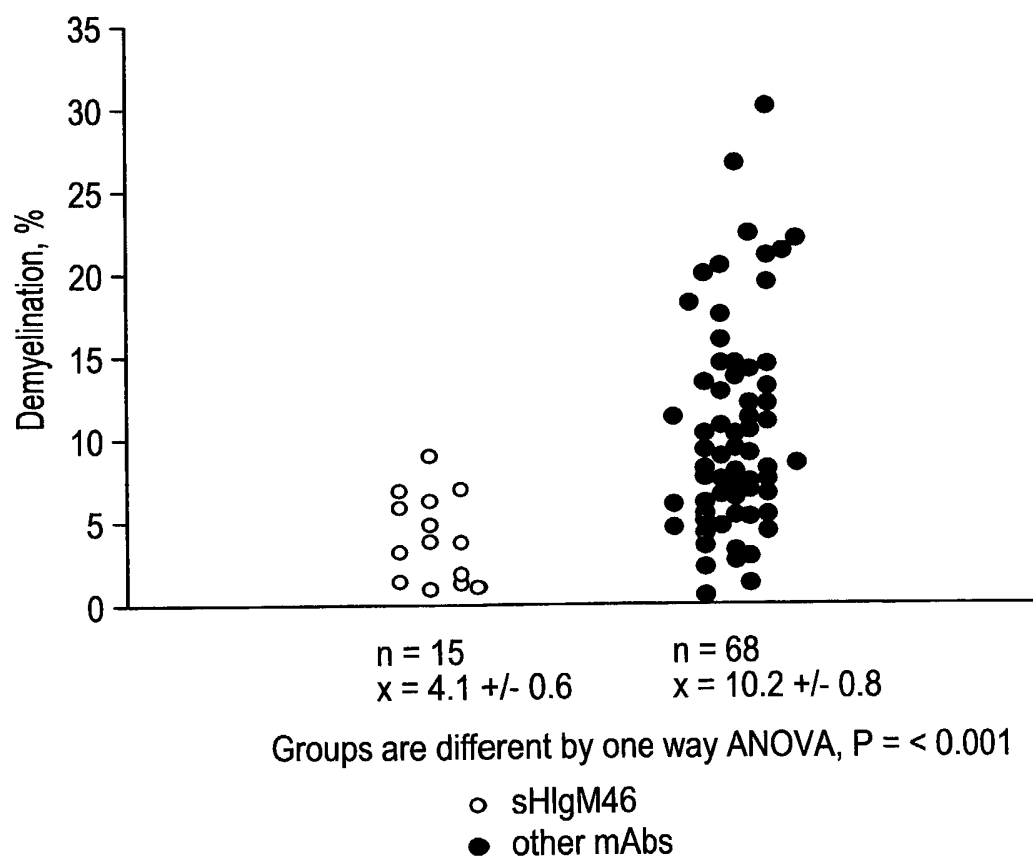


Chronically TMEV Infected SJL Mice Treated with sHlgM46 or sHlgM22





Chronically TMEV Infected SJL Mice Treated sHlgM46 vs All Other Antibodies



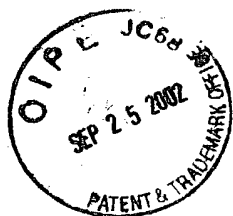
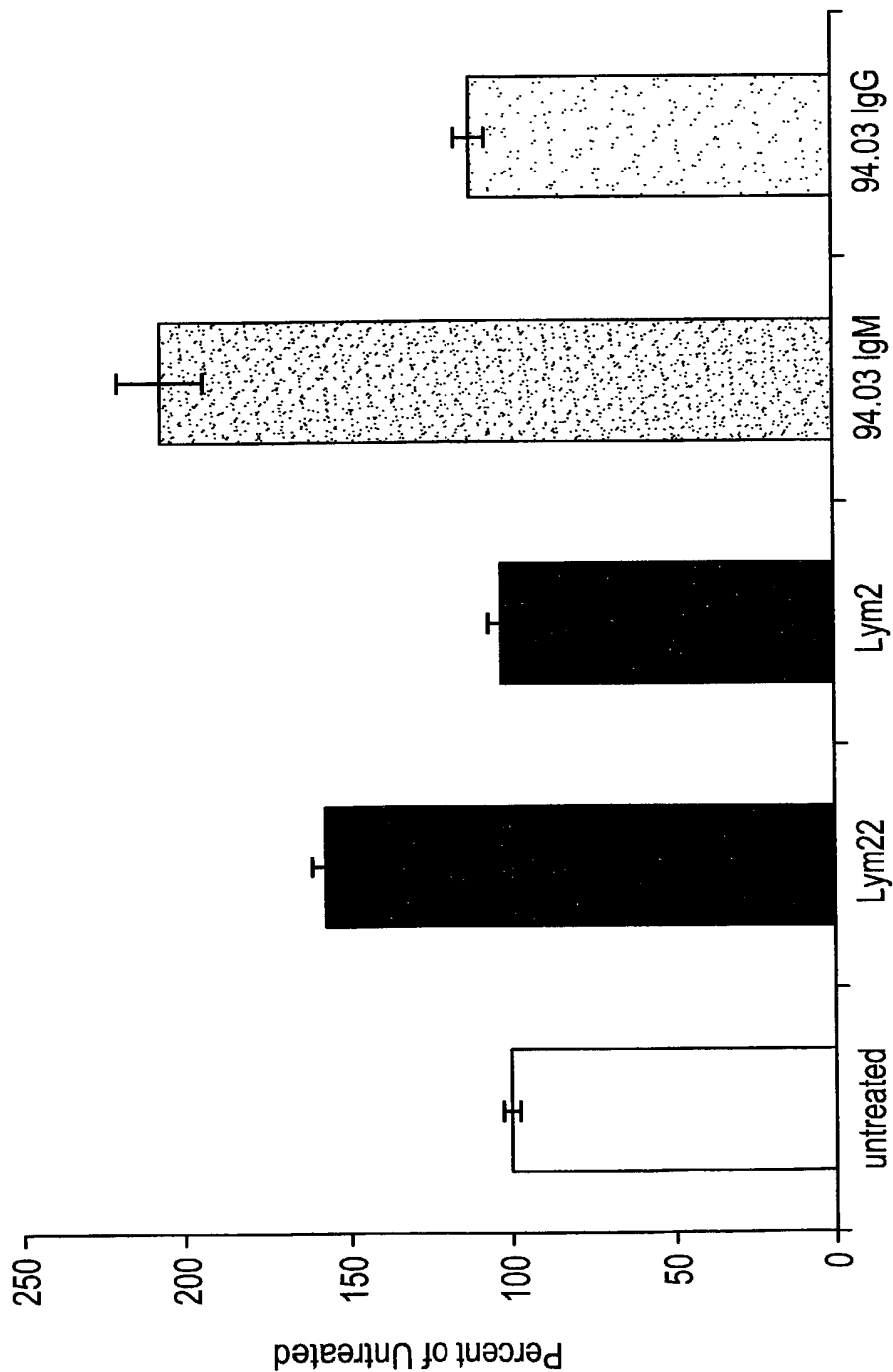


FIG. 83

^{45}Ca Internalization in Undif CG4 Cells



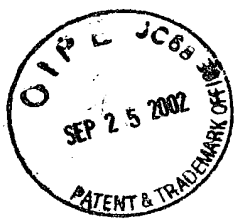
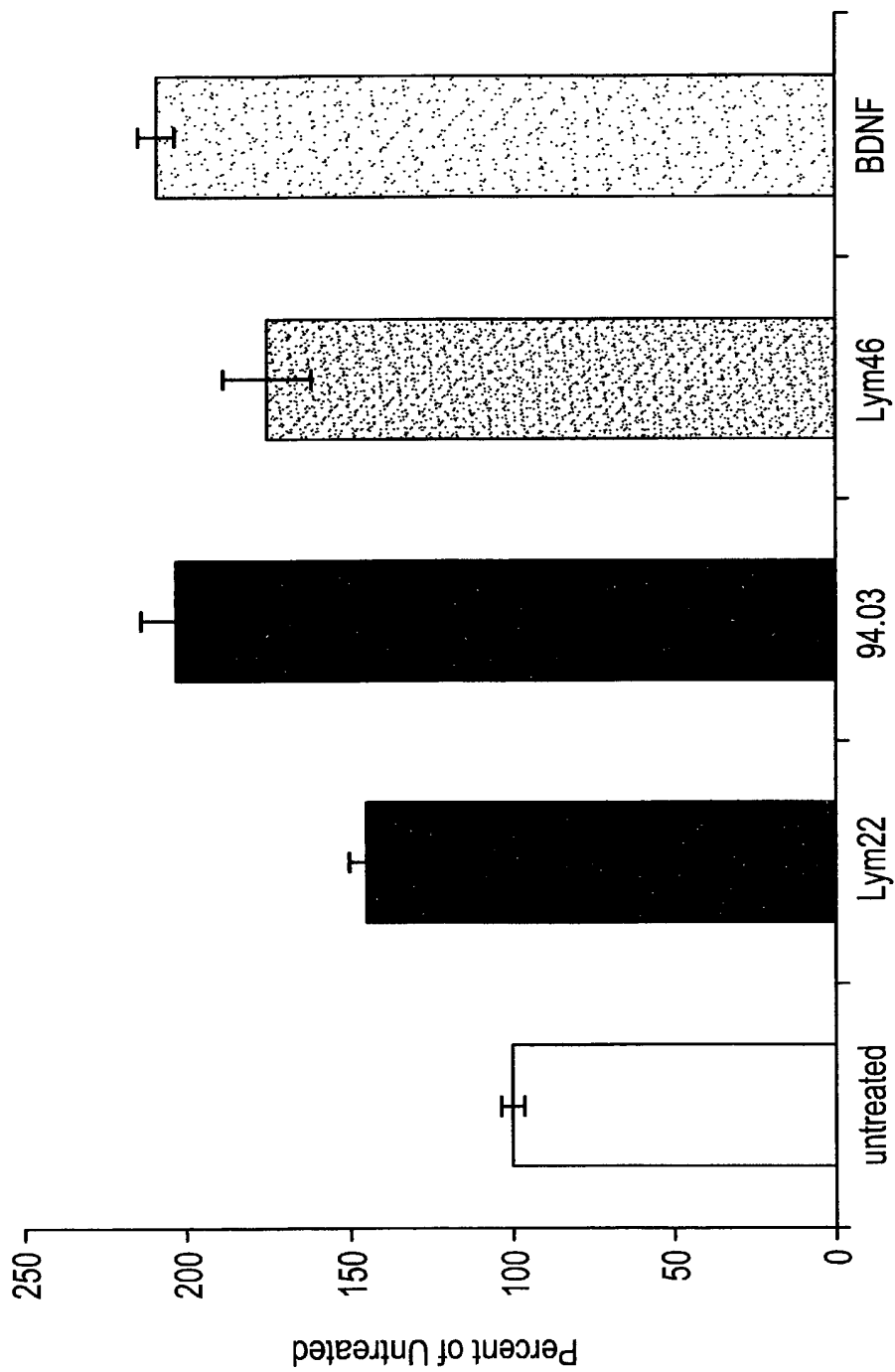


FIG. 84

^{45}Ca Internalization in CG4 Cells



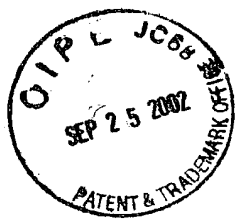
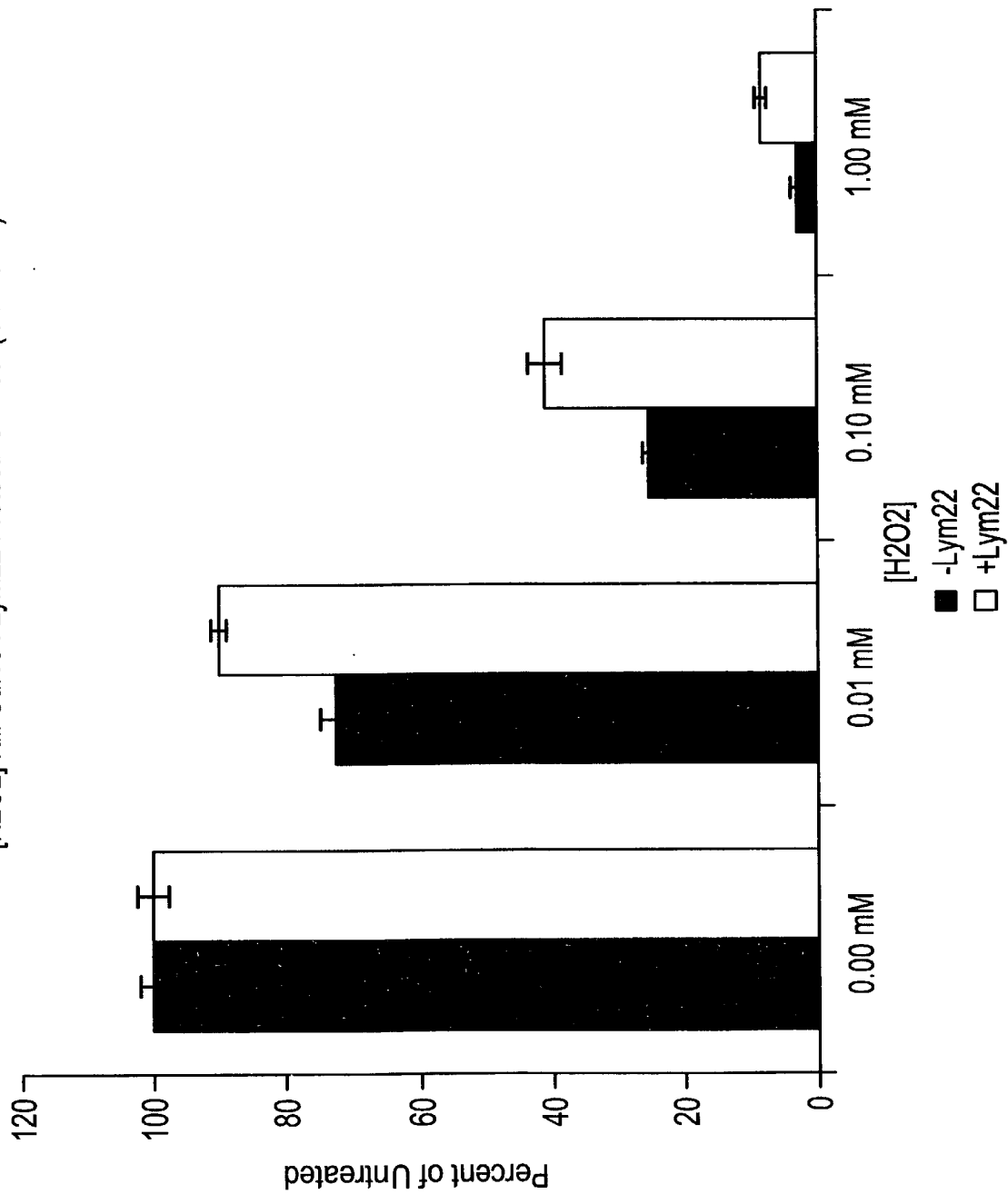


FIG. 85

[H₂O₂] Kill Curve : Lym22 Protective Effect (CG4 cells)



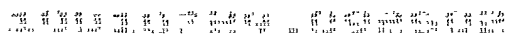


FIG. 86A

MTT Assay: H₂O₂-induced cell death

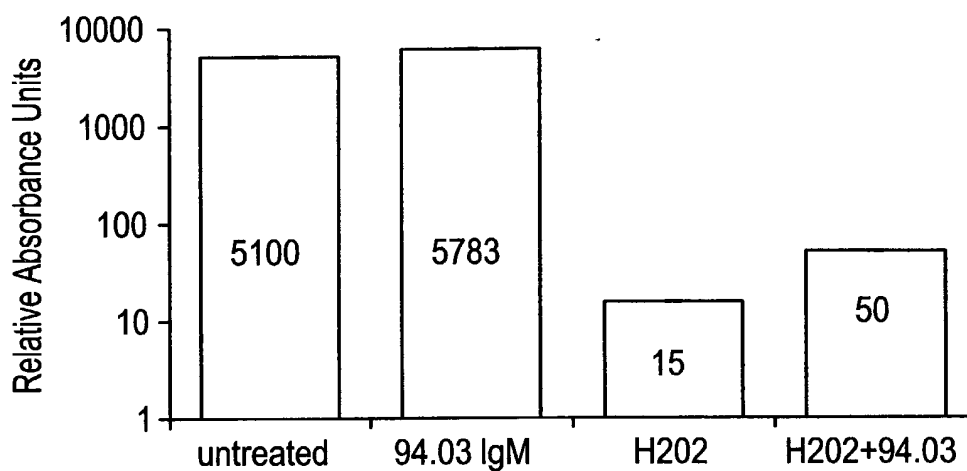


FIG. 86B

Cell Number: H₂O₂-induced cell death

